www.biovirus.org

- Elliot Lefkowitz - UAB
- Chris Upton - UVic

Viral Bioinformatics Resource Center

& Viral Bioinformatics - Canada

University of Victoria

Workbench
- VOCS
- VGO
- Base By Base
- JDotter
- ReHAB
- GFS
- NAP
- GraphDNA
- Hydrophobicity
- Codon Statistics

Web Tools
- Laj Gallery
- BLAST
- EMBOSS

Information
- About Us
- About VBCa
- Virus Families
- Workbench
- Requirements

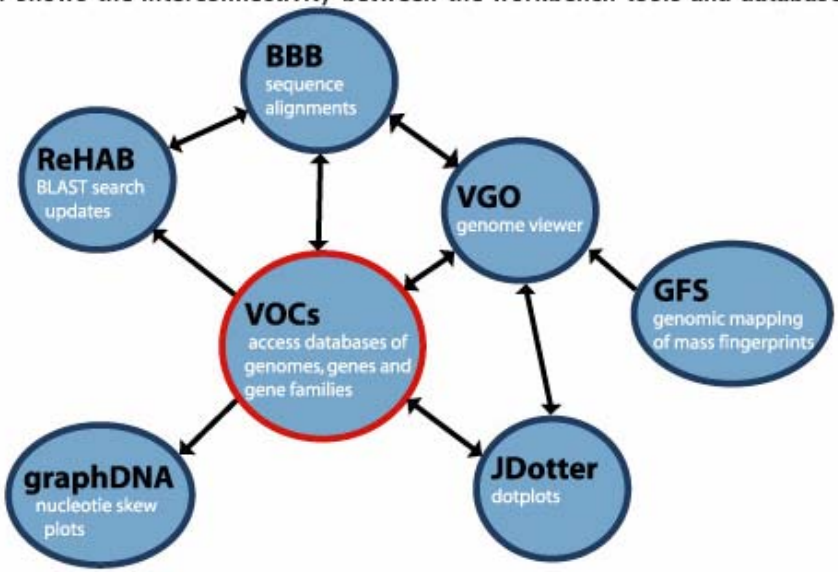
Welcome

This resource
Provides access to viral genomes and a variety tools for comparative genomic analyses. At the heart of the system is VOCs (Virus Orthologous Clusters), a database with built-in tools that allows users to retrieve and analyze the genes, gene families, and genomes of 11 different virus families. The database is the source of information for other programs of the workbench for whole genome alignments, genome display, or gene/protein sequence analysis. Many of these tools can also be used with user-provided sequence data. The workbench tools are Java-based and user-friendly to allow all users, regardless of computer skill-level, to access and analyze the data.

To start
There are two ways to start an application from the workbench:

- Select an application, and then choose its associated database when the application starts.
- Select a database, and then start an application using the afore-selected database.

The figure below shows the interconnectivity between the workbench tools and databases at VBCa



Databases

dsDNA viruses
- Adenoviridae
- Baculoviridae
- Herpesviridae
- Poxviridae

+ ssRNA viruses
- Coronaviridae
- Flaviviridae
- Togaviridae

- ssRNA viruses
- Arenaviridae
- Bunyaviridae
- Filoviridae
- Paramyxoviridae

Bacterial plasmids
- Plasmids

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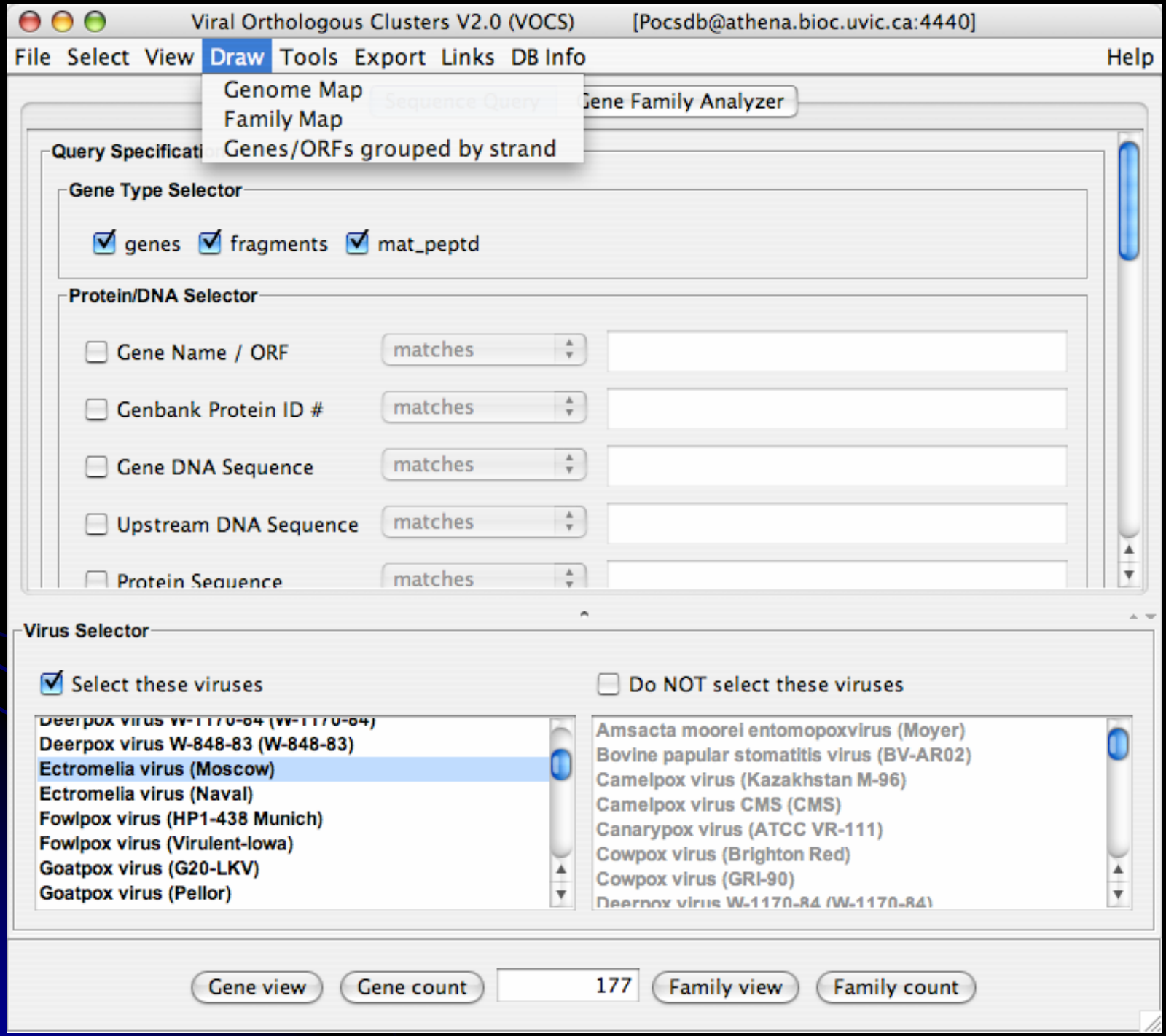
Viral Genome Comparisons

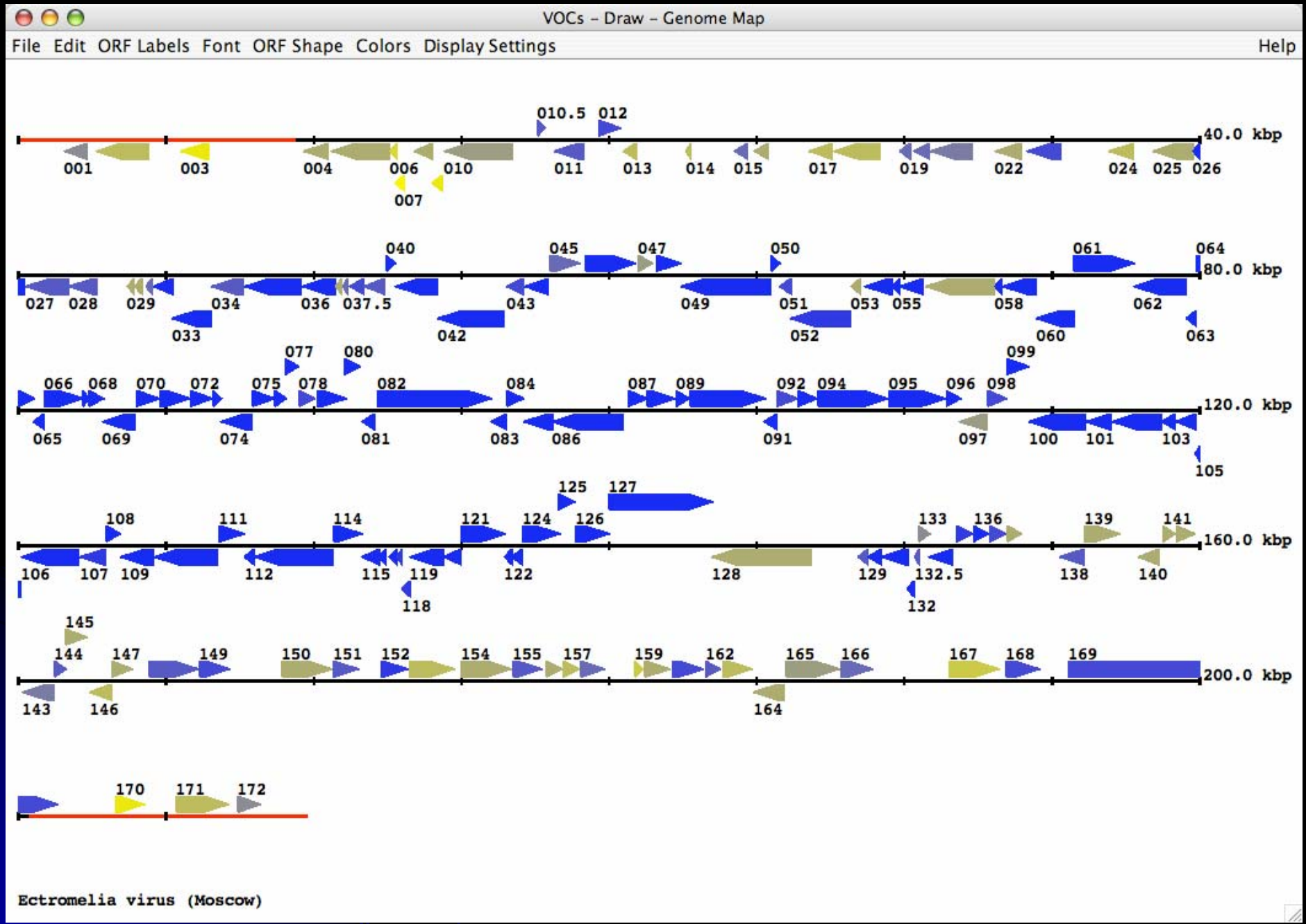
- Virus Orthologous clusters (VOCs)
- JDotter
- Viral Genome Organizer (VGO)
- Base-By-Base
- DNA Grapher

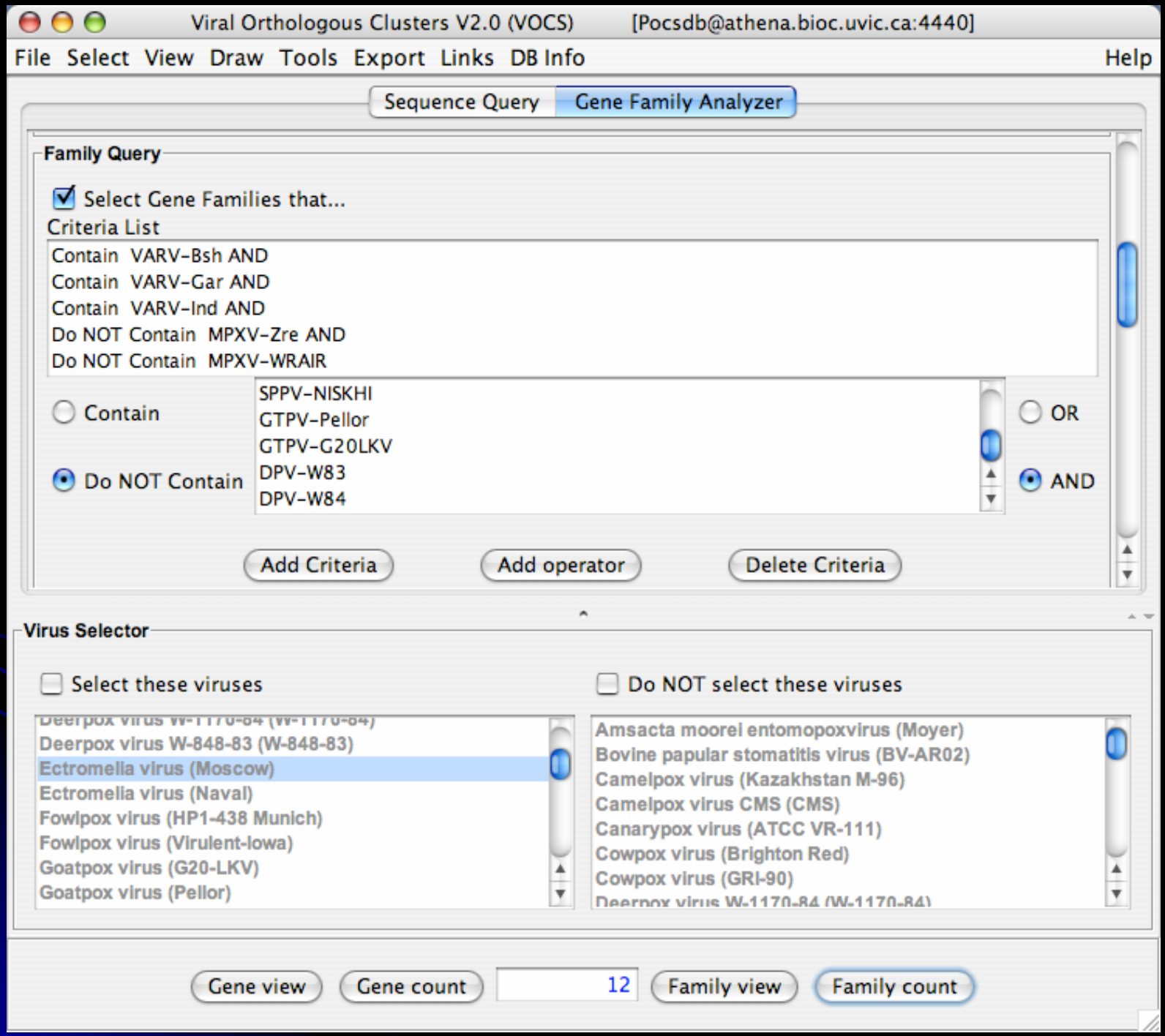
Viral Orthologous Clusters

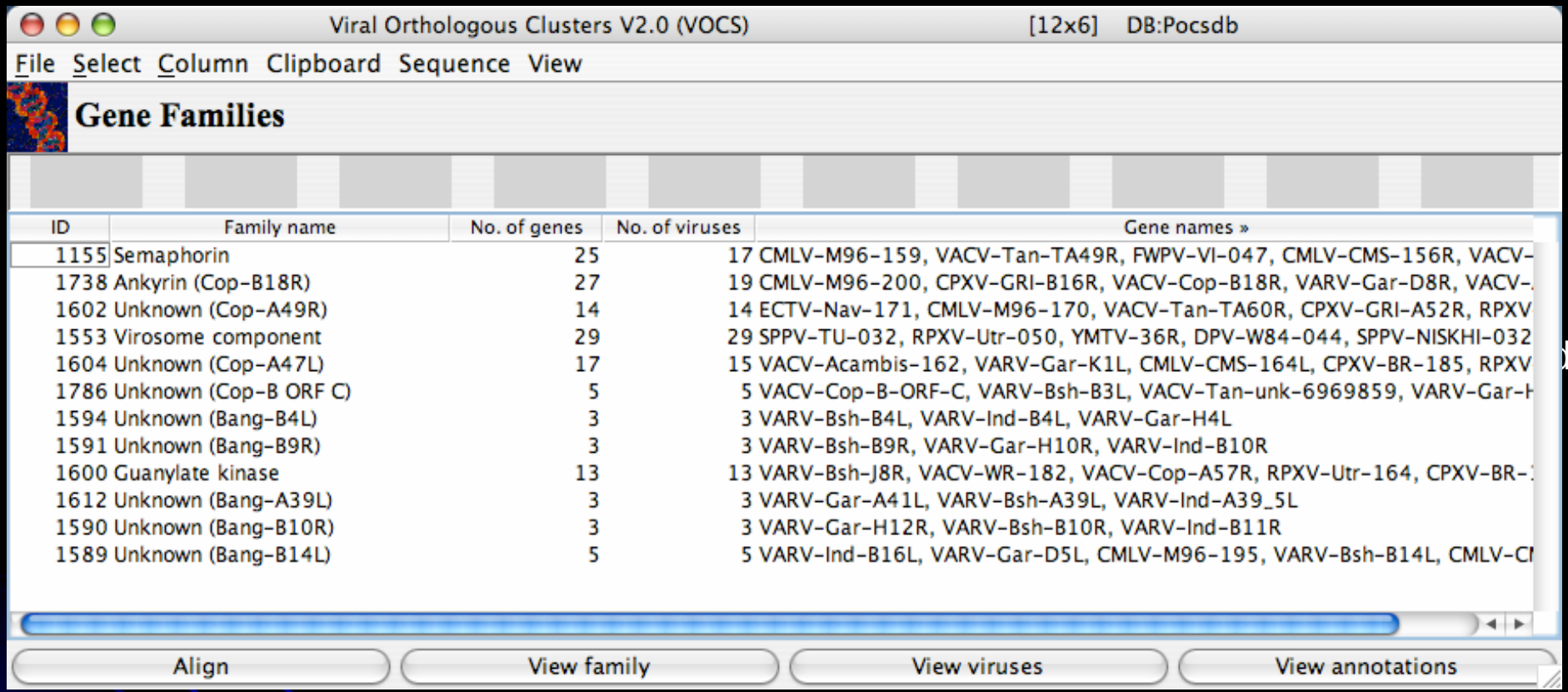
VOCS

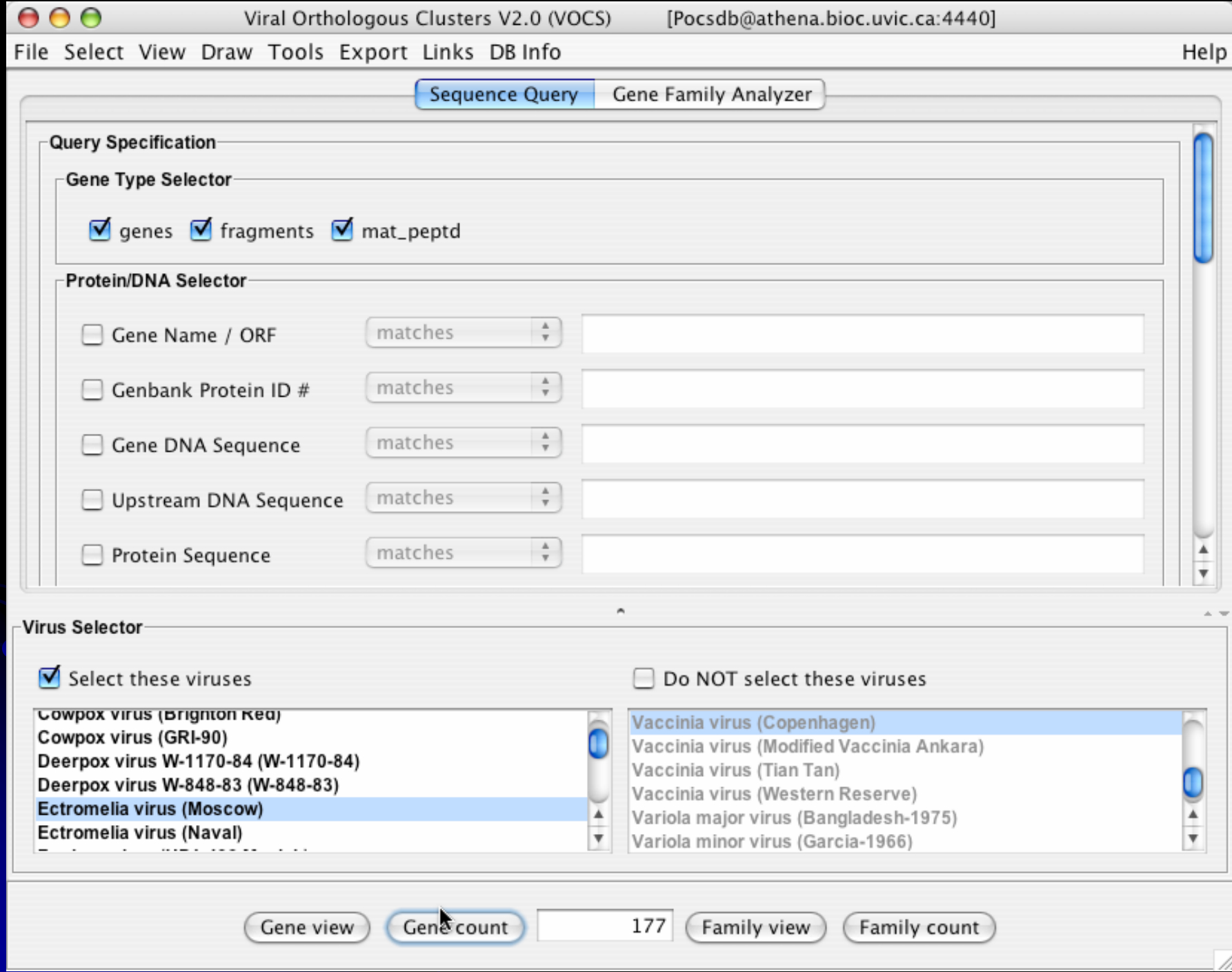
- Database
  - Viral genomes, genes, proteins, annotations
  - Grouped into families of orthologs
- Resource for all other software
  - 1st step in work-flow


Viral Orthologous Clusters V2.0 (VOCS)
[Pocsdb@athena.bioc.uvic.ca:4440]
File Select View Draw Tools Export Links DB Info Help
Genome Map
Family Map
Genes/ORFs grouped by strand
Sequence Query
Gene Family Analyzer
Query Specificati
Gene Type Selector
genes
fragments
mat_peptd
Protein/DNA Selector
Gene Name / ORF
matches
Genbank Protein ID #
matches
Gene DNA Sequence
matches
Upstream DNA Sequence
matches
Protein Sequence
matches
Virus Selector
Select these viruses
Do NOT select these viruses
Deerpox virus W-1170-84 (W-1170-84)
Deerpox virus W-848-83 (W-848-83)
Ectromelia virus (Moscow)
Ectromelia virus (Naval)
Fowlpox virus (HP1-438 Munich)
Fowlpox virus (Virulent-Iowa)
Goatpox virus (G20-LKV)
Goatpox virus (Pellor)
Amsacta moorei entomopoxvirus (Moyer)
Bovine papular stomatitis virus (BV-AR02)
Camelpox virus (Kazakhstan M-96)
Camelpox virus CMS (CMS)
Canarypox virus (ATCC VR-111)
Cowpox virus (Brighton Red)
Cowpox virus (GRI-90)
Deerpox virus W-1170-84 (W-1170-84)
Gene view
Gene count
177
Family view
Family count


VOCs – Draw – Genome Map
File Edit ORF Labels Font ORF Shape Colors Display Settings Help
40.0 kbp
80.0 kbp
120.0 kbp
160.0 kbp
200.0 kbp
Ectromelia virus (Moscow)


Viral Orthologous Clusters V2.0 (VOCS)
[Pocsdb@athena.bioc.uvic.ca:4440]
File Select View Draw Tools Export Links DB Info Help
Sequence Query
Gene Family Analyzer
Family Query
Select Gene Families that...
Criteria List
Contain VARV-Bsh AND
Contain VARV-Gar AND
Contain VARV-Ind AND
Do NOT Contain MPXV-Zre AND
Do NOT Contain MPXV-WRAIR
Contain
Do NOT Contain
SPPV-NISKHI
GTPV-Pellor
GTPV-G20LKV
DPV-W83
DPV-W84
OR
AND
Add Criteria
Add operator
Delete Criteria
Virus Selector
Select these viruses
Do NOT select these viruses
Deerpox virus W-848-83 (W-848-83)
Ectromelia virus (Moscow)
Ectromelia virus (Naval)
Fowlpox virus (HP1-438 Munich)
Fowlpox virus (Virulent-Iowa)
Goatpox virus (G20-LKV)
Goatpox virus (Pellor)
Amsacta moorei entomopoxvirus (Moyer)
Bovine papular stomatitis virus (BV-AR02)
Camelpox virus (Kazakhstan M-96)
Camelpox virus CMS (CMS)
Canarypox virus (ATCC VR-111)
Cowpox virus (Brighton Red)
Cowpox virus (GRI-90)
Gene view
Gene count
12
Family view
Family count


Viral Orthologous Clusters V2.0 (VOCS) [12x6] DB:Pocsdb
File Select Column Clipboard Sequence View
Gene Families
ID Family name No. of genes No. of viruses Gene names »
1155 Semaphorin 25 17 CMLV-M96-159, VACV-Tan-TA49R, FWPV-VI-047, CMLV-CMS-156R, VACV-
1738 Ankyrin (Cop-B18R) 27 19 CMLV-M96-200, CPXV-GRI-B16R, VACV-Cop-B18R, VARV-Gar-D8R, VACV-
1602 Unknown (Cop-A49R) 14 14 ECTV-Nav-171, CMLV-M96-170, VACV-Tan-TA60R, CPXV-GRI-A52R, RPXV
1553 Virosome component 29 29 SPPV-TU-032, RPXV-Utr-050, YMTV-36R, DPV-W84-044, SPPV-NISKHI-032
1604 Unknown (Cop-A47L) 17 15 VACV-Acambis-162, VARV-Gar-K1L, CMLV-CMS-164L, CPXV-BR-185, RPXV
1786 Unknown (Cop-B ORF C) 5 5 VACV-Cop-B-ORF-C, VARV-Bsh-B3L, VACV-Tan-unk-6969859, VARV-Gar-
1594 Unknown (Bang-B4L) 3 3 VARV-Bsh-B4L, VARV-Ind-B4L, VARV-Gar-H4L
1591 Unknown (Bang-B9R) 3 3 VARV-Bsh-B9R, VARV-Gar-H10R, VARV-Ind-B10R
1600 Guanylate kinase 13 13 VARV-Bsh-J8R, VACV-WR-182, VACV-Cop-A57R, RPXV-Utr-164, CPXV-BR-
1612 Unknown (Bang-A39L) 3 3 VARV-Gar-A41L, VARV-Bsh-A39L, VARV-Ind-A39_5L
1590 Unknown (Bang-B10R) 3 3 VARV-Gar-H12R, VARV-Bsh-B10R, VARV-Ind-B11R
1589 Unknown (Bang-B14L) 5 5 VARV-Ind-B16L, VARV-Gar-D5L, CMLV-M96-195, VARV-Bsh-B14L, CMLV-C
Align
View family
View viruses
View annotations


Viral Orthologous Clusters V2.0 (VOCS) [Pocsdb@athena.bioc.uvic.ca:4440]
File Select View Draw Tools Export Links DB Info Help
Sequence Query
Gene Family Analyzer
Query Specification
Gene Type Selector
genes
fragments
mat_peptd
Protein/DNA Selector
Gene Name / ORF
matches
Genbank Protein ID #
matches
Gene DNA Sequence
matches
Upstream DNA Sequence
matches
Protein Sequence
matches
Virus Selector
Select these viruses
Do NOT select these viruses
Cowpox virus (Brighton Red)
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Deerpox virus W-1170-84 (W-1170-84)
Deerpox virus W-848-83 (W-848-83)
Ectromelia virus (Moscow)
Ectromelia virus (Naval)
Vaccinia virus (Copenhagen)
Vaccinia virus (Modified Vaccinia Ankara)
Vaccinia virus (Tian Tan)
Vaccinia virus (Western Reserve)
Variola major virus (Bangladesh-1975)
Variola minor virus (Garcia-1966)
Gene view
Gene count
177
Family view
Family count

Viral Orthologous Clusters V2.0 (VOCS) [177x12] DB:Pocsdb

File Select Column Clipboard Sequence Blast Alignment Analysis JDotter

Gene Results Table

Gene name	Family name	ORF start	ORF stop	ORF strandedness	Fragment	Adenine + Thymin...	pI	No. of amino acids
ECTV-Mos-001	Chemokine binding protein	1580	2323	bottom	no	56.45	4.68	247
ECTV-Mos-002	Ankyrin (Cop-B25R)	2652	4415	bottom	no	62.19	7.62	587
ECTV-Mos-003	TNF receptor (CrmD)	5506	6468	bottom	no	62.21	5.34	320
ECTV-Mos-004	Kelch-like (Cop-A55R)	9673	10494	bottom	no	65.45	4.53	273
ECTV-Mos-005	Ankyrin (Bang-B18R)	10613	12565	bottom	no	69.33	5.53	650
ECTV-Mos-006	C-type lectin (FPV-V-008)	12597	12824	bottom	no	67.98	6.69	75
ECTV-Mos-007	CPV-B-012	12766	13077	bottom	no	69.87	9.08	103
ECTV-Mos-008	TNF receptor (CrmB)	13411	14019	bottom	yes	66.17	4.41	202
ECTV-Mos-009	Unknown (CPXV-GRI-D13L)	14016	14351	bottom	yes	62.50	7.89	111
ECTV-Mos-010	Ankyrin (Cop-B18R)	14442	16733	bottom	no	67.67	5.91	763
ECTV-Mos-011	IL-1 Receptor antagonist	18154	19149	bottom	no	69.08	4.68	331
ECTV-Mos-012	Ubiquitin Ligase	19658	20383	top	no	68.73	8.79	241
ECTV-Mos-013	IL-18 BP (C12L)	20499	20915	bottom	no	62.35	5.09	138
ECTV-Mos-014	Unknown (Tan-TC10L)	22603	22782	bottom	no	57.78	10.12	59
ECTV-Mos-015	Host range virulence factor	24248	24700	bottom	no	67.10	6.43	150
ECTV-Mos-016	Unknown (Cop-C6L)	24924	25391	bottom	no	65.81	4.87	155
ECTV-Mos-017	Complement binding (secreted)	26776	27564	bottom	no	59.45	8.22	262
ECTV-Mos-018	Kelch-like (Cop-C2L)	27620	29158	bottom	no	68.16	8.67	512
ECTV-Mos-019	Virokine (Cop-N1L)	29846	30199	bottom	no	66.10	4.74	117
ECTV-Mos-020	Alpha-amanitin sensitivity	30328	30861	bottom	no	66.48	6.95	177
ECTV-Mos-021	Ankyrin (Cop-M1L)	30894	32312	bottom	no	67.37	5.74	472
ECTV-Mos-022	Ankyrin/Host range (Cop-K1L)	33087	33944	bottom	no	65.04	6.17	285
ECTV-Mos-023	Serpin (SPI)	34170	35291	bottom	no	64.35	6.96	373
ECTV-Mos-024	Putative monoglyceride lipase	36932	37765	bottom	no	64.03	8.21	277
ECTV-Mos-025	Apoptosis inhibitor (mitochondri...	38419	39789	bottom	no	69.22	3.70	456
ECTV-Mos-026	dUTPase	39789	40232	bottom	no	63.06	7.73	147
ECTV-Mos-027	Kelch-like (Cop-F3L)	40260	41708	bottom	no	66.32	8.27	482
ECTV-Mos-028	Ribonucleotide Reductase small...	41719	42678	bottom	no	65.42	4.92	319
ECTV-Mos-029	Unknown (Cop-F6L)	43703	43927	bottom	no	69.33	4.52	74
ECTV-Mos-030	Unknown (Cop-F7L)	43942	44190	bottom	no	65.06	5.40	82
ECTV-Mos-031	Cytoplasmic protein (Cop-F8L)	44331	44528	bottom	no	60.10	9.25	65

Display Family Annotations Sequences Coding Regions

Viral Orthologous Clusters V2.0 (VOCS) [177x12] DB:Pocsdb

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ECTV-Mos-030	Unknown (Cop-F7L)	43942	44190	bottom	no	65.06	5.40	82
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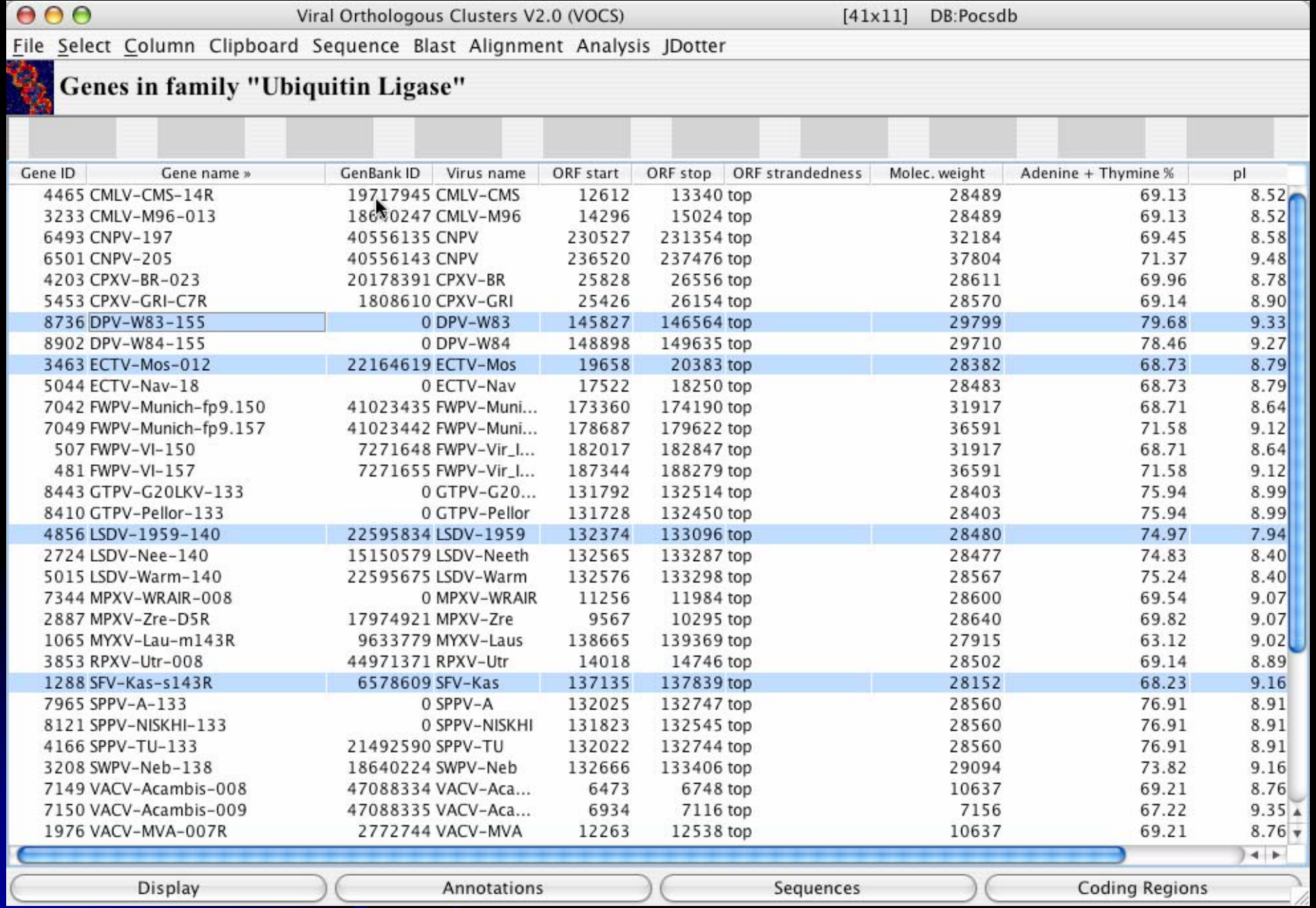
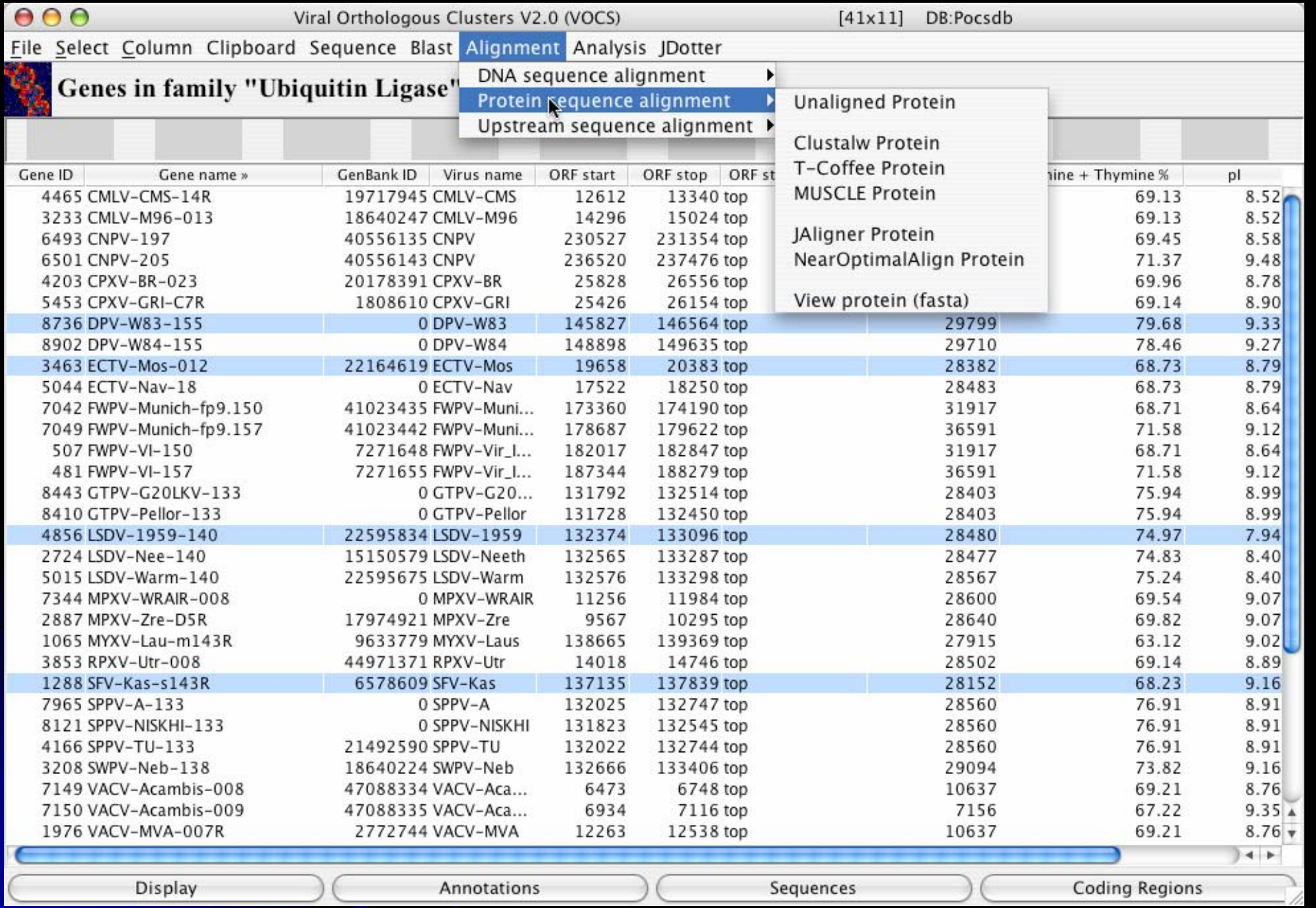
Display | Family | Annotations | Sequences | Coding Regions


Viral Orthologous Clusters V2.0 (VOCS) [41x11] DB:Pocsdb
File Select Column Clipboard Sequence Blast Alignment Analysis JDotter
Genes in family "Ubiquitin Ligase"
Gene ID Gene name » GenBank ID Virus name ORF start ORF stop ORF strandedness Molec. weight Adenine + Thymine % pI
4465 CMLV-CMS-14R 19717945 CMLV-CMS 12612 13340 top 28489 69.13 8.52
3233 CMLV-M96-013 18600247 CMLV-M96 14296 15024 top 28489 69.13 8.52
6493 CNPV-197 40556135 CNPV 230527 231354 top 32184 69.45 8.58
6501 CNPV-205 40556143 CNPV 236520 237476 top 37804 71.37 9.48
4203 CPXV-BR-023 20178391 CPXV-BR 25828 26556 top 28611 69.96 8.78
5453 CPXV-GRI-C7R 1808610 CPXV-GRI 25426 26154 top 28570 69.14 8.90
8736 DPV-W83-155 0 DPV-W83 145827 146564 top 29799 79.68 9.33
8902 DPV-W84-155 0 DPV-W84 148898 149635 top 29710 78.46 9.27
3463 ECTV-Mos-012 22164619 ECTV-Mos 19658 20383 top 28382 68.73 8.79
5044 ECTV-Nav-18 0 ECTV-Nav 17522 18250 top 28483 68.73 8.79
7042 FWPV-Munich-fp9.150 41023435 FWPV-Muni... 173360 174190 top 31917 68.71 8.64
7049 FWPV-Munich-fp9.157 41023442 FWPV-Muni... 178687 179622 top 36591 71.58 9.12
507 FWPV-VI-150 7271648 FWPV-Vir_I... 182017 182847 top 31917 68.71 8.64
481 FWPV-VI-157 7271655 FWPV-Vir_I... 187344 188279 top 36591 71.58 9.12
8443 GTPV-G20LKV-133 0 GTPV-G20... 131792 132514 top 28403 75.94 8.99
8410 GTPV-Pellor-133 0 GTPV-Pellor 131728 132450 top 28403 75.94 8.99
4856 LSDV-1959-140 22595834 LSDV-1959 132374 133096 top 28480 74.97 7.94
2724 LSDV-Nee-140 15150579 LSDV-Neeth 132565 133287 top 28477 74.83 8.40
5015 LSDV-Warm-140 22595675 LSDV-Warm 132576 133298 top 28567 75.24 8.40
7344 MPXV-WRAIR-008 0 MPXV-WRAIR 11256 11984 top 28600 69.54 9.07
2887 MPXV-Zre-D5R 17974921 MPXV-Zre 9567 10295 top 28640 69.82 9.07
1065 MYXV-Lau-m143R 9633779 MYXV-Laus 138665 139369 top 27915 63.12 9.02
3853 RPXV-Utr-008 44971371 RPXV-Utr 14018 14746 top 28502 69.14 8.89
1288 SFV-Kas-s143R 6578609 SFV-Kas 137135 137839 top 28152 68.23 9.16
7965 SPPV-A-133 0 SPPV-A 132025 132747 top 28560 76.91 8.91
8121 SPPV-NISKHI-133 0 SPPV-NISKHI 131823 132545 top 28560 76.91 8.91
4166 SPPV-TU-133 21492590 SPPV-TU 132022 132744 top 28560 76.91 8.91
3208 SWPV-Neb-138 18640224 SWPV-Neb 132666 133406 top 29094 73.82 9.16
7149 VACV-Acambis-008 47088334 VACV-Aca... 6473 6748 top 10637 69.21 8.76
7150 VACV-Acambis-009 47088335 VACV-Aca... 6934 7116 top 7156 67.22 9.35
1976 VACV-MVA-007R 2772744 VACV-MVA 12263 12538 top 10637 69.21 8.76
Display
Annotations
Sequences
Coding Regions


Viral Orthologous Clusters V2.0 (VOCS)
[41x11]
DB:Pocsdb
File Select Column Clipboard Sequence Blast Alignment Analysis JDotter
Genes in family "Ubiquitin Ligase"
DNA sequence alignment
Protein sequence alignment
Upstream sequence alignment
Unaligned Protein
Clustalw Protein
T-Coffee Protein
MUSCLE Protein
JAligner Protein
NearOptimalAlign Protein
View protein (fasta)
Gene ID
Gene name »
GenBank ID
Virus name
ORF start
ORF stop
ORF st
Thymine %
pI
4465 CMLV-CMS-14R 19717945 CMLV-CMS 12612 13340 top 69.13 8.52
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4203 CPXV-BR-023 20178391 CPXV-BR 25828 26556 top 69.96 8.78
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8736 DPV-W83-155 0 DPV-W83 145827 146564 top 29799 79.68 9.33
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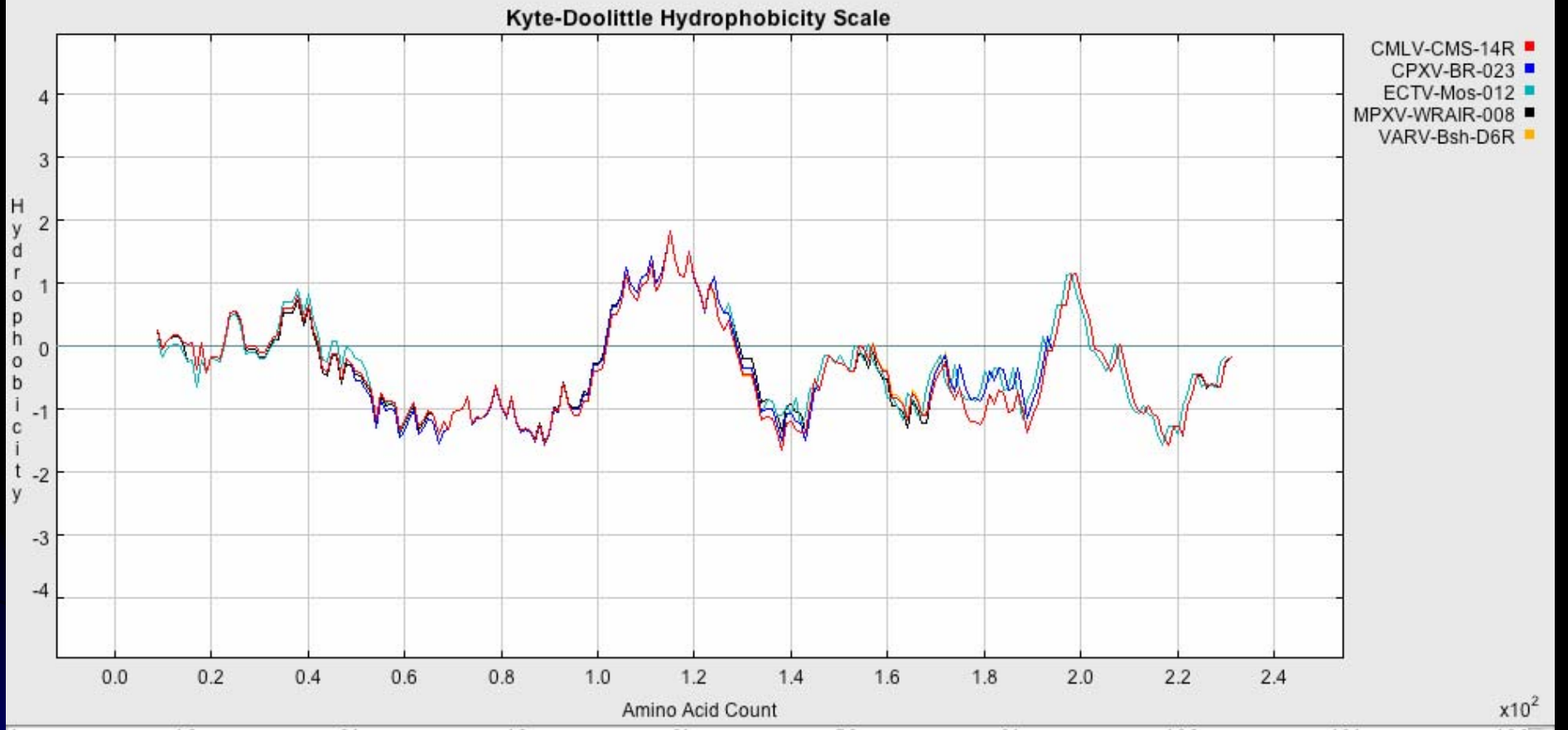
4856 LSDV-1959-140 22595834 LSDV-1959 132374 133096 top 28480 74.97 7.94
2724 LSDV-Nee-140 15150579 LSDV-Neeth 132565 133287 top 28477 74.83 8.40
5015 LSDV-Warm-140 22595675 LSDV-Warm 132576 133298 top 28567 75.24 8.40
7344 MPXV-WRAIR-008 0 MPXV-WRAIR 11256 11984 top 28600 69.54 9.07
2887 MPXV-Zre-D5R 17974921 MPXV-Zre 9567 10295 top 28640 69.82 9.07
1065 MYXV-Lau-m143R 9633779 MYXV-Laus 138665 139369 top 27915 63.12 9.02
3853 RPXV-Utr-008 44971371 RPXV-Utr 14018 14746 top 28502 69.14 8.89
1288 SFV-Kas-s143R 6578609 SFV-Kas 137135 137839 top 28152 68.23 9.16
7965 SPPV-A-133 0 SPPV-A 132025 132747 top 28560 76.91 8.91
8121 SPPV-NISKHI-133 0 SPPV-NISKHI 131823 132545 top 28560 76.91 8.91
4166 SPPV-TU-133 21492590 SPPV-TU 132022 132744 top 28560 76.91 8.91
3208 SWPV-Neb-138 18640224 SWPV-Neb 132666 133406 top 29094 73.82 9.16
7149 VACV-Acambis-008 47088334 VACV-Aca... 6473 6748 top 10637 69.21 8.76
7150 VACV-Acambis-009 47088335 VACV-Aca... 6934 7116 top 7156 67.22 9.35
1976 VACV-MVA-007R 2772744 VACV-MVA 12263 12538 top 10637 69.21 8.76
Display
Annotations
Sequences
Coding Regions

VOCS - Hydrophobicity-Plotter

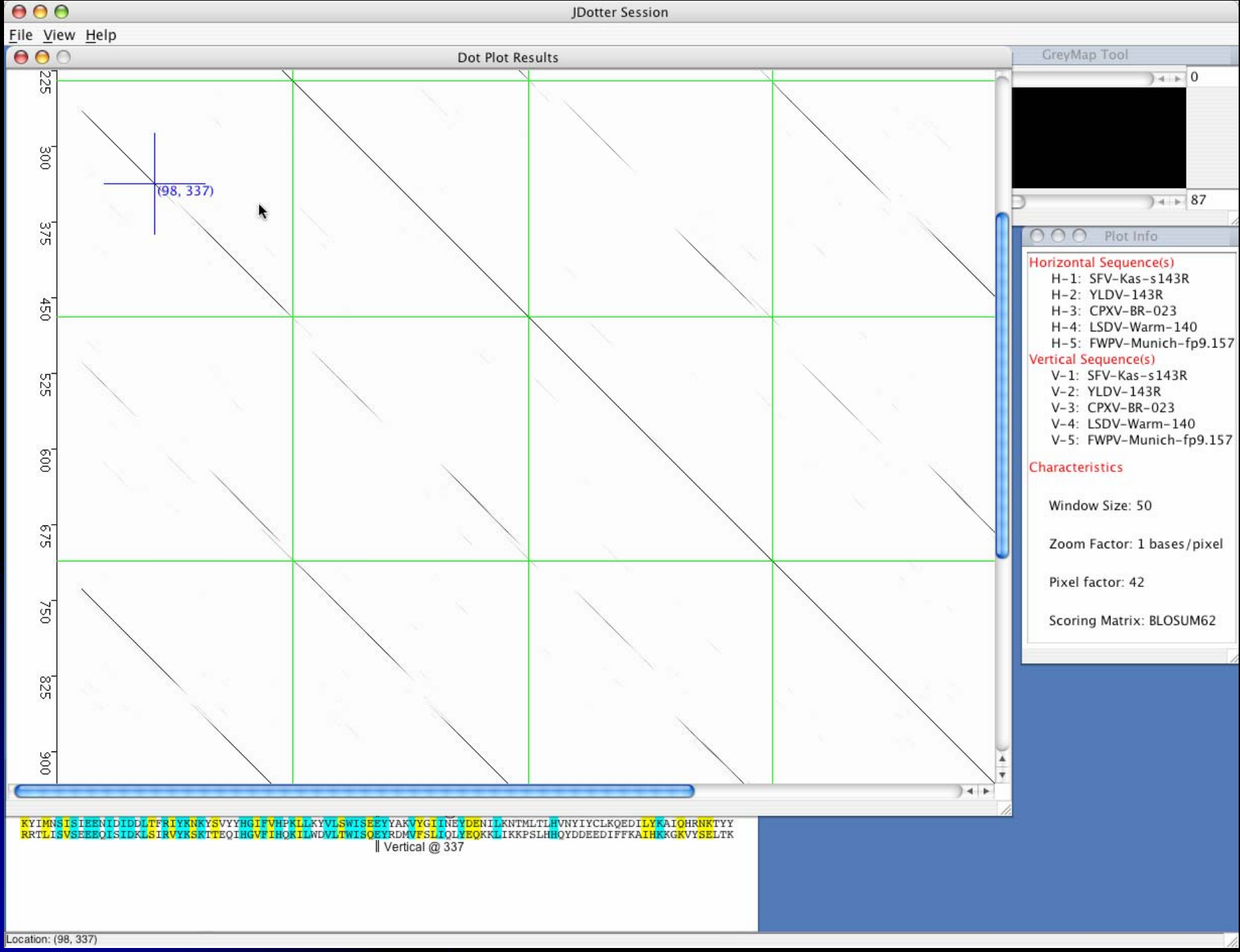
File View Help

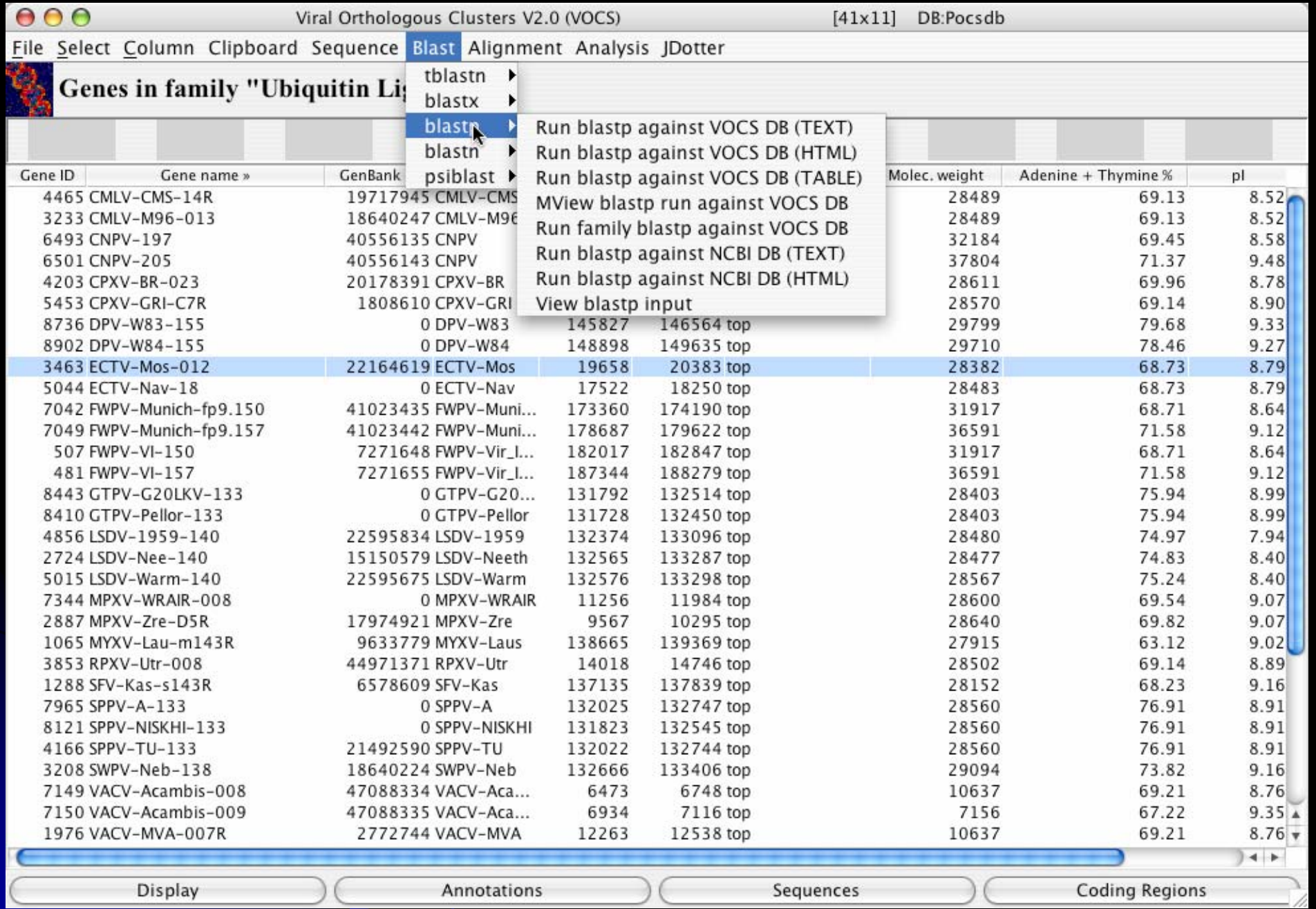
Window Size: 19 Scale System: Kyte-Doolittle Replot




```
1          16         31         46         61         76         91         106        121        136
MEFDPSKINISSIDHVTILQYIDEPNDIRLTVCIIQNINNITYYINITKINPHLANQFRAWKKRIAGRDYMTNLSRDTGIQQSNLTETIRNCQKNRNIYGLYIHHNLVINLVIDWITDVIVQSIVRGLVNWYIDNNTY
MEFDPTKINISSIDHVTILQYIDEPNDIRLTVCIIQNINNITYYINITKINPHLANQFRTWKKRIAGRDYMTNLSRDTGIQQSKLTETIRNCQKNRNIYGLYIHYNLVINVVIDWITDVIVQSILRGLVNWYIANNNY
MEFDPAKINTSSIDHVTILQYIDEPNDIRLPVCIIRNINNITYFINITKINPDLANQFRAWKKRIAGRDYMTNLSRDTGIQQSKLTETIRNCQKNRNIYGLYIHYNLVINVVIDWITDVIVQSILRGLVNWYIANNTY
```

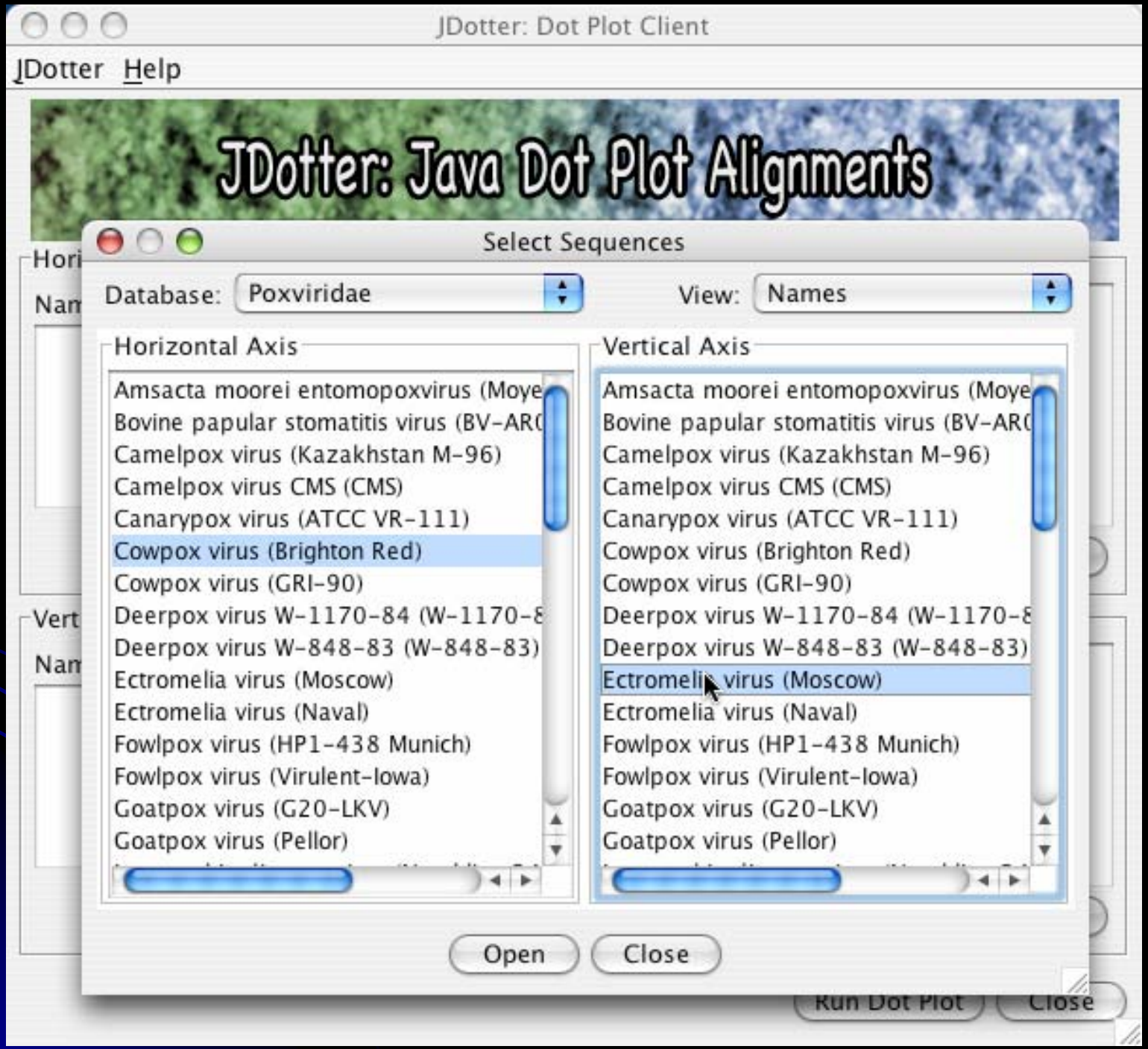
Close Window Reset View

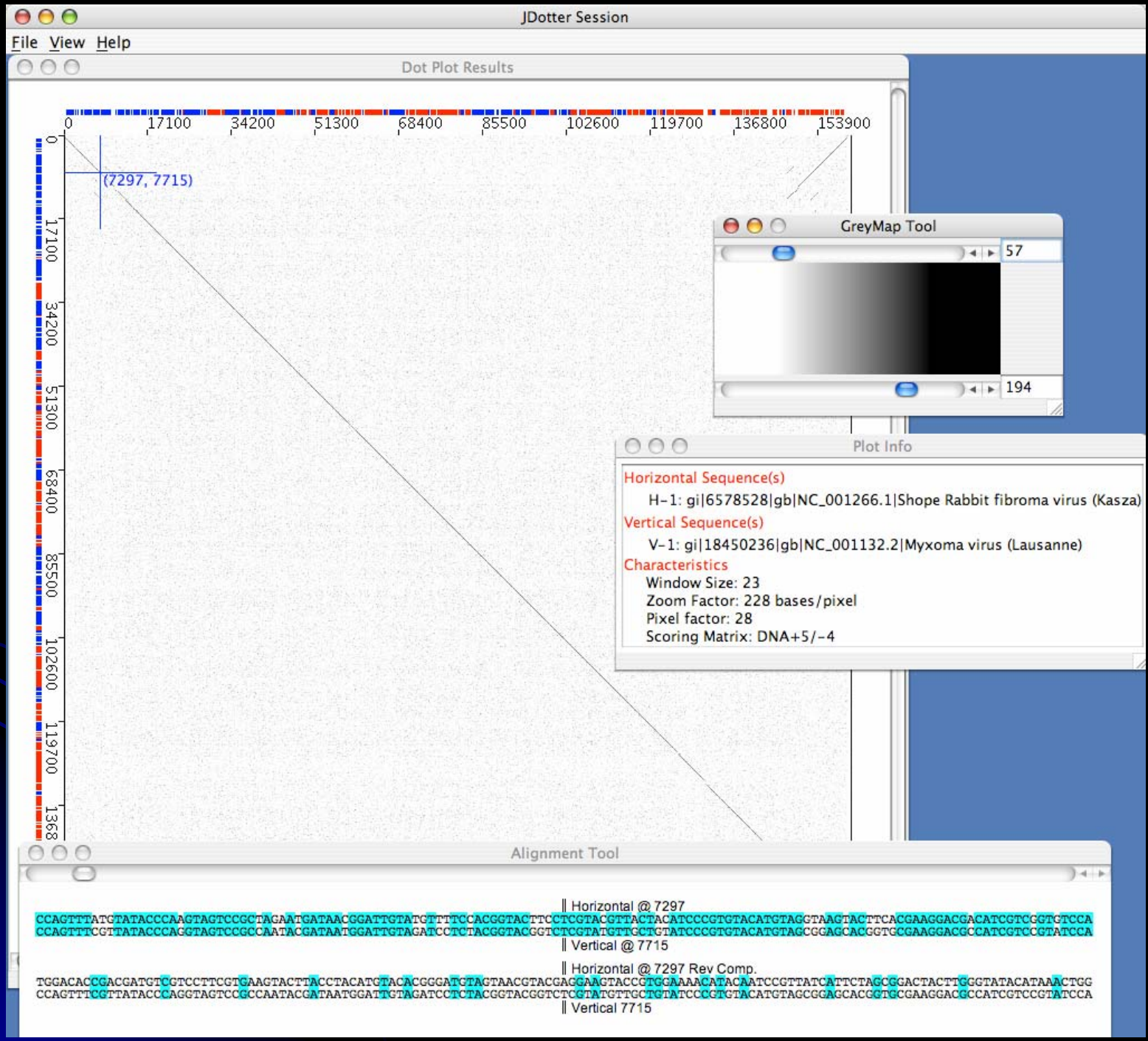

JDotter Session
File View Help
Dot Plot Results
GreyMap Tool
0
87
Plot Info
Horizontal Sequence(s)
H-1: SFV-Kas-s143R
H-2: YLDV-143R
H-3: CPXV-BR-023
H-4: LSDV-Warm-140
H-5: FWPV-Munich-fp9.157
Vertical Sequence(s)
V-1: SFV-Kas-s143R
V-2: YLDV-143R
V-3: CPXV-BR-023
V-4: LSDV-Warm-140
V-5: FWPV-Munich-fp9.157
Characteristics
Window Size: 50
Zoom Factor: 1 bases/pixel
Pixel factor: 42
Scoring Matrix: BLOSUM62
225
300
375
450
525
600
675
750
825
900
(98, 337)
KYIMNSISIEENIDIDDLTFRIYKNKYSVYYHGIFVHPKLLKYVLSWISEEYYAKVYGIINEYDENILKNTMLTLHVNYIYCLKQEDILYKAIQHRNKTYY
RRTLISVSEEEQISIDKLSIRVYKSKTTEQIHGVFIHQKILWDVLTWISQEYRDMVFSLIQLYEQKKLIKKPSLHHQYDDEEDIFFKAIHKKGKVYSELTK
Vertical @ 337
Location: (98, 337)

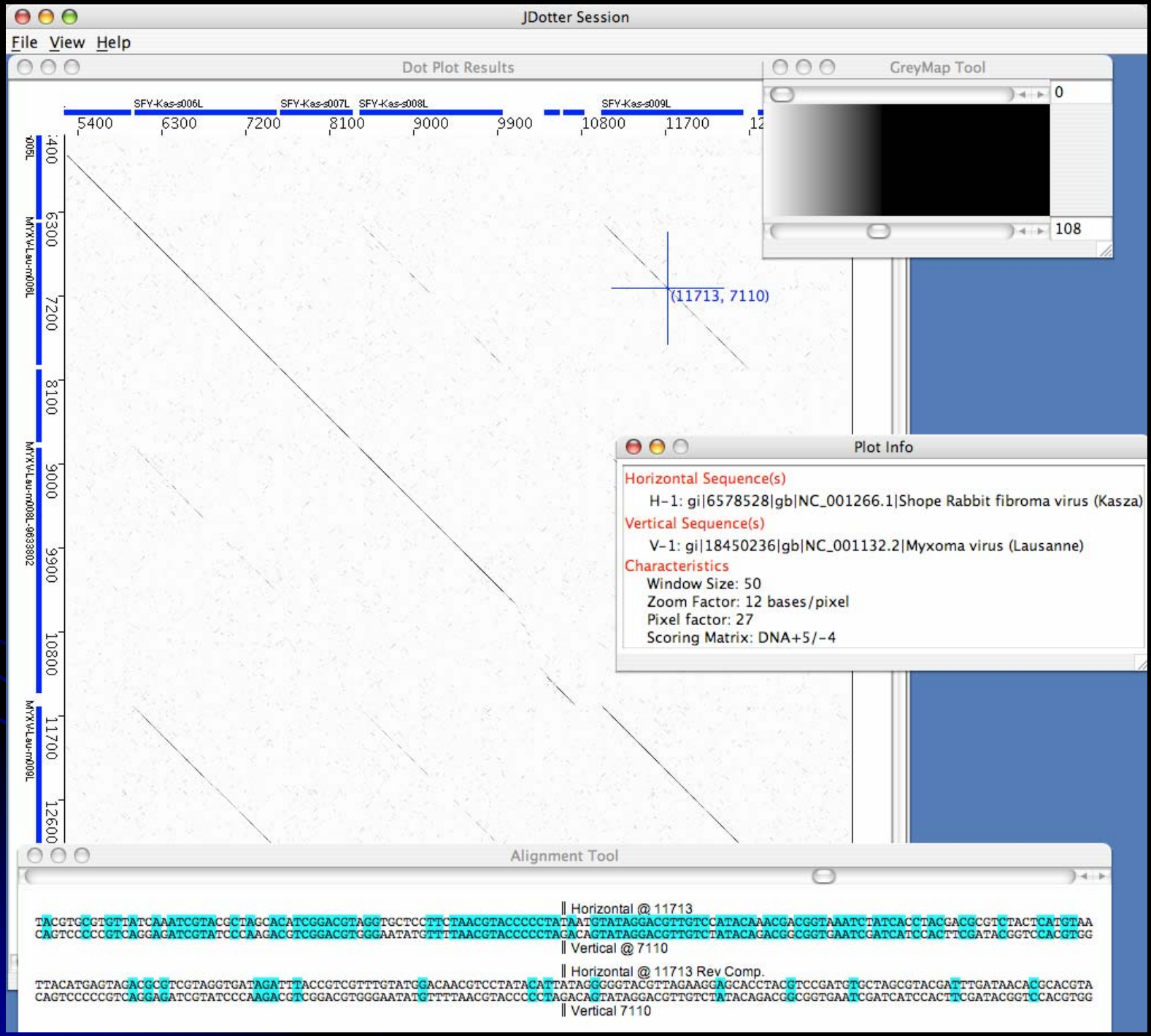

Viral Orthologous Clusters V2.0 (VOCS) [41x11] DB:Pocsdb
File Select Column Clipboard Sequence Blast Alignment Analysis JDotter
Genes in family "Ubiquitin Lig
tblastn
blastx
blastp
blastn
psiblast
Run blastp against VOCS DB (TEXT)
Run blastp against VOCS DB (HTML)
Run blastp against VOCS DB (TABLE)
MView blastp run against VOCS DB
Run family blastp against VOCS DB
Run blastp against NCBI DB (TEXT)
Run blastp against NCBI DB (HTML)
View blastp input
Gene ID Gene name » GenBank Molec. weight Adenine + Thymine % pI
4465 CMLV-CMS-14R 19717945 CMLV-CMS 28489 69.13 8.52
3233 CMLV-M96-013 18640247 CMLV-M96 28489 69.13 8.52
6493 CNPV-197 40556135 CNPV 32184 69.45 8.58
6501 CNPV-205 40556143 CNPV 37804 71.37 9.48
4203 CPXV-BR-023 20178391 CPXV-BR 28611 69.96 8.78
5453 CPXV-GRI-C7R 1808610 CPXV-GRI 28570 69.14 8.90
8736 DPV-W83-155 0 DPV-W83 145827 146564 top 29799 79.68 9.33
8902 DPV-W84-155 0 DPV-W84 148898 149635 top 29710 78.46 9.27
3463 ECTV-Mos-012 22164619 ECTV-Mos 19658 20383 top 28382 68.73 8.79
5044 ECTV-Nav-18 0 ECTV-Nav 17522 18250 top 28483 68.73 8.79
7042 FWPV-Munich-fp9.150 41023435 FWPV-Muni... 173360 174190 top 31917 68.71 8.64
7049 FWPV-Munich-fp9.157 41023442 FWPV-Muni... 178687 179622 top 36591 71.58 9.12
507 FWPV-VI-150 7271648 FWPV-Vir_I... 182017 182847 top 31917 68.71 8.64
481 FWPV-VI-157 7271655 FWPV-Vir_I... 187344 188279 top 36591 71.58 9.12
8443 GTPV-G20LKV-133 0 GTPV-G20... 131792 132514 top 28403 75.94 8.99
8410 GTPV-Pellor-133 0 GTPV-Pellor 131728 132450 top 28403 75.94 8.99
4856 LSDV-1959-140 22595834 LSDV-1959 132374 133096 top 28480 74.97 7.94
2724 LSDV-Nee-140 15150579 LSDV-Neeth 132565 133287 top 28477 74.83 8.40
5015 LSDV-Warm-140 22595675 LSDV-Warm 132576 133298 top 28567 75.24 8.40
7344 MPXV-WRAIR-008 0 MPXV-WRAIR 11256 11984 top 28600 69.54 9.07
2887 MPXV-Zre-D5R 17974921 MPXV-Zre 9567 10295 top 28640 69.82 9.07
1065 MYXV-Lau-m143R 9633779 MYXV-Laus 138665 139369 top 27915 63.12 9.02
3853 RPXV-Utr-008 44971371 RPXV-Utr 14018 14746 top 28502 69.14 8.89
1288 SFV-Kas-s143R 6578609 SFV-Kas 137135 137839 top 28152 68.23 9.16
7965 SPPV-A-133 0 SPPV-A 132025 132747 top 28560 76.91 8.91
8121 SPPV-NISKHI-133 0 SPPV-NISKHI 131823 132545 top 28560 76.91 8.91
4166 SPPV-TU-133 21492590 SPPV-TU 132022 132744 top 28560 76.91 8.91
3208 SWPV-Neb-138 18640224 SWPV-Neb 132666 133406 top 29094 73.82 9.16
7149 VACV-Acambis-008 47088334 VACV-Aca... 6473 6748 top 10637 69.21 8.76
7150 VACV-Acambis-009 47088335 VACV-Aca... 6934 7116 top 7156 67.22 9.35
1976 VACV-MVA-007R 2772744 VACV-MVA 12263 12538 top 10637 69.21 8.76
Display
Annotations
Sequences
Coding Regions

JDotter: Java Dot Plot Alignments

- Java front end to Dotter
  - Sonnhammer,E.L. and Durbin,R. (1995) A dot-matrix program with dynamic threshold control suited for genomic DNA and protein sequence analysis. *Gene*, **167**, GC1-GC10
- Platform independent (client-server)
- Preprocessed dotplots
- Local screen refreshing
- Zoom-replotting performed on server
- Displays gene annotations from VOCs


JDotter: Dot Plot Client
JDotter Help
JDotter: Java Dot Plot Alignments
Select Sequences
Database: Poxviridae
View: Names
Horizontal Axis
Vertical Axis
Amsacta moorei entomopoxvirus (Moye
Bovine papular stomatitis virus (BV-AR(
Camelpox virus (Kazakhstan M-96)
Camelpox virus CMS (CMS)
Canarypox virus (ATCC VR-111)
Cowpox virus (Brighton Red)
Cowpox virus (GRI-90)
Deerpox virus W-1170-84 (W-1170-8
Deerpox virus W-848-83 (W-848-83)
Ectromelia virus (Moscow)
Ectromelia virus (Naval)
Fowlpox virus (HP1-438 Munich)
Fowlpox virus (Virulent-Iowa)
Goatpox virus (G20-LKV)
Goatpox virus (Pellor)
Open
Close
Run Dot Plot
Close

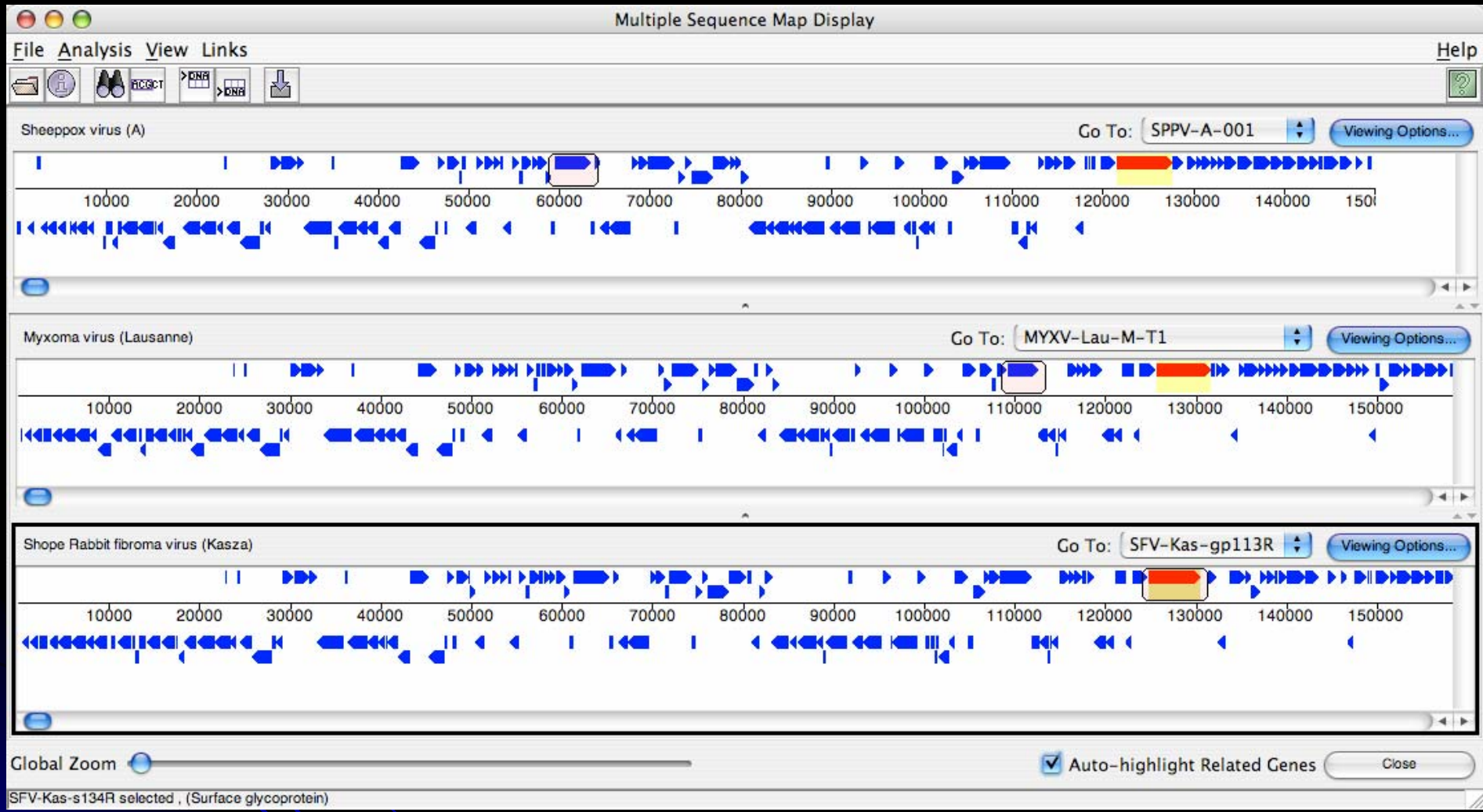

JDotter Session
File View Help
Dot Plot Results
0
17100
34200
51300
68400
85500
102600
119700
136800
153900
(7297, 7715)
GreyMap Tool
57
194
Plot Info
Horizontal Sequence(s)
H-1: gi|6578528|gb|NC_001266.1|Shope Rabbit fibroma virus (Kasza)
Vertical Sequence(s)
V-1: gi|18450236|gb|NC_001132.2|Myxoma virus (Lausanne)
Characteristics
Window Size: 23
Zoom Factor: 228 bases/pixel
Pixel factor: 28
Scoring Matrix: DNA+5/-4
Alignment Tool
Horizontal @ 7297
CCAGTTTATGTATACCCAAGTAGTCCGCTAGAATGATAACGGATTGTATGTTTTCCACGGTACTTCCTCGTACGTTACTACATCCCGTGTACATGTAGGTAAGTACTTCACGAAGGACGACATCGTCGGTGTCCA
CCAGTTTCGTTATACCCAGGTAGTCCGCCAATACGATAATGGATTGTAGATCCTCTACGGTACGGTCTCGTATGTTGCTGTATCCCGTGTACATGTAGCGGAGCACGGTGCGAAGGACGCCATCGTCCGTATCCA
Vertical @ 7715
Horizontal @ 7297 Rev Comp.
TGGACACCGACGATGTCGTCCTTCGTGAAGTACTTACCTACATGTACACGGGATCTAGTAACGTACGAGGAAGTACCGTGGAAAACATACAATCCGTTATCATTCTAGCGGACTACTTGGGTATACATAAACTGG
CCAGTTTCGTTATACCCAGGTAGTCCGCCAATACGATAATGGATTGTAGATCCTCTACGGTACGGTCTCGTATGTTGCTGTATCCCGTGTACATGTAGCGGAGCACGGTGCGAAGGACGCCATCGTCCGTATCCA
Vertical 7715


JDotter Session
File View Help
Dot Plot Results
SFY-Kas-s006L
SFY-Kas-s007L
SFY-Kas-s008L
SFY-Kas-s009L
5400
6300
7200
8100
9000
9900
10800
11700
6300
7200
8100
9000
9900
10800
11700
12600
(11713, 7110)
GreyMap Tool
0
108
Plot Info
Horizontal Sequence(s)
H-1: gi|6578528|gb|NC_001266.1|Shope Rabbit fibroma virus (Kasza)
Vertical Sequence(s)
V-1: gi|18450236|gb|NC_001132.2|Myxoma virus (Lausanne)
Characteristics
Window Size: 50
Zoom Factor: 12 bases/pixel
Pixel factor: 27
Scoring Matrix: DNA+5/-4
Alignment Tool
‖ Horizontal @ 11713
TACGTGCGTGTTATCAAATCGTACGCTAGCACATCGGACGTAGGTGCTCCTTCTAACGTACCCCCTATAATGTATAGGACGTTGTCCATACAAACGACGGTAAATCTATCACCTACGACGCGTCTACTCATGTAA
CAGTCCCCCGTCAGGAGATCGTATCCCAAGACGTCGGACGTGGGAATATGTTTTAACGTACCCCCTAGACAGTATAGGACGTTGTCTATACAGACGGCGGTGAATCGATCATCCACTTCGATACGGTCCACGTGG
‖ Vertical @ 7110
‖ Horizontal @ 11713 Rev Comp.
TTACATGAGTAGACGCGTCGTAGGTGATAGATTTACCGTCGTTTGTATGGACAACGTCCTATACATTATAGGGGTACGTTAGAAGGAGCACCTACGTCCGATGTGCTAGCGTACGATTTGATAACACGCACGTA
CAGTCCCCCGTCAGGAGATCGTATCCCAAGACGTCGGACGTGGGAATATGTTTTAACGTACCCCCTAGACAGTATAGGACGTTGTCTATACAGACGGCGGTGAATCGATCATCCACTTCGATACGGTCCACGTGG
‖ Vertical 7110

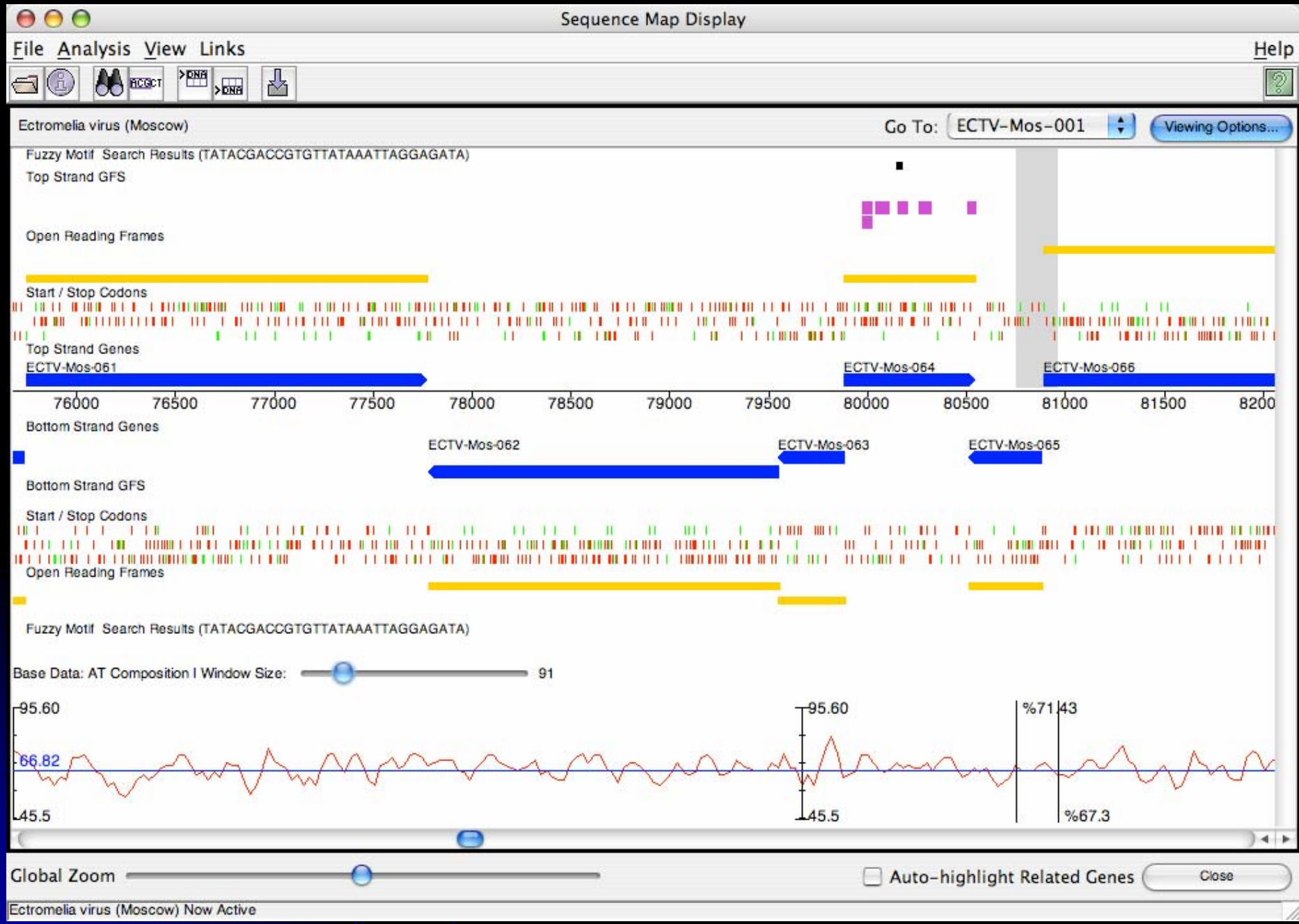
Viral Genome Organizer

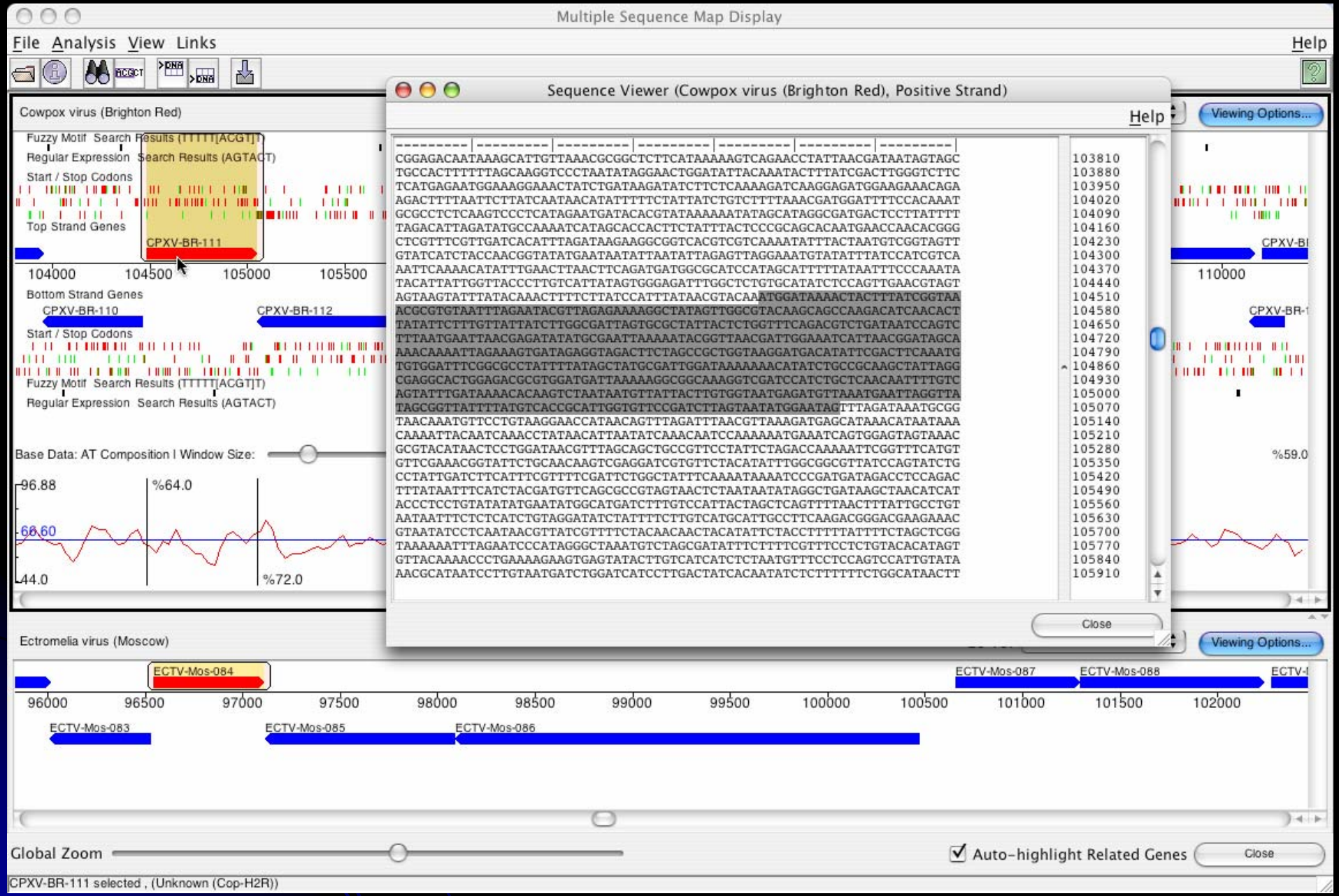
VGO

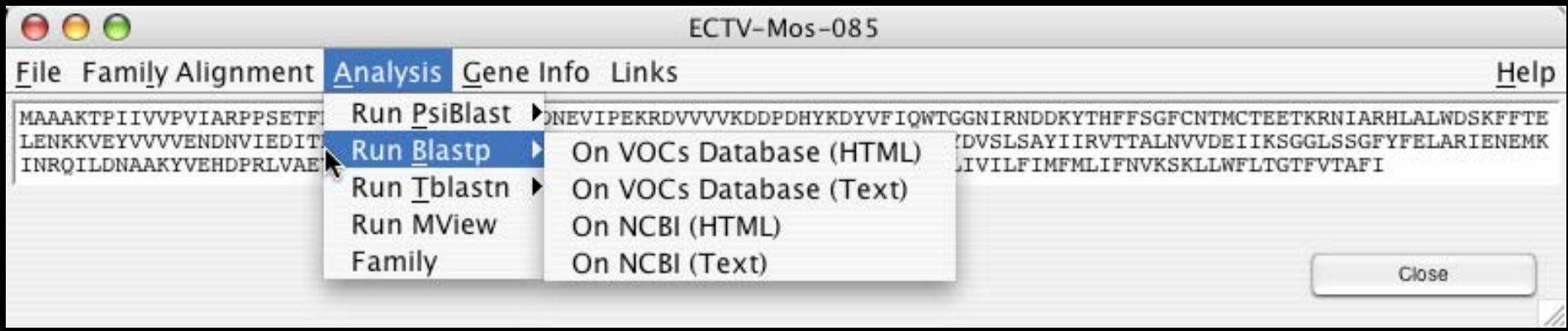
- Graphical genome viewer
  - Multiple genomes
  - Uses VOCs database to display orthologs
  - Access to protein and DNA sequences
  - Displays results from other tools



- Ortholog data from curated VOCs database

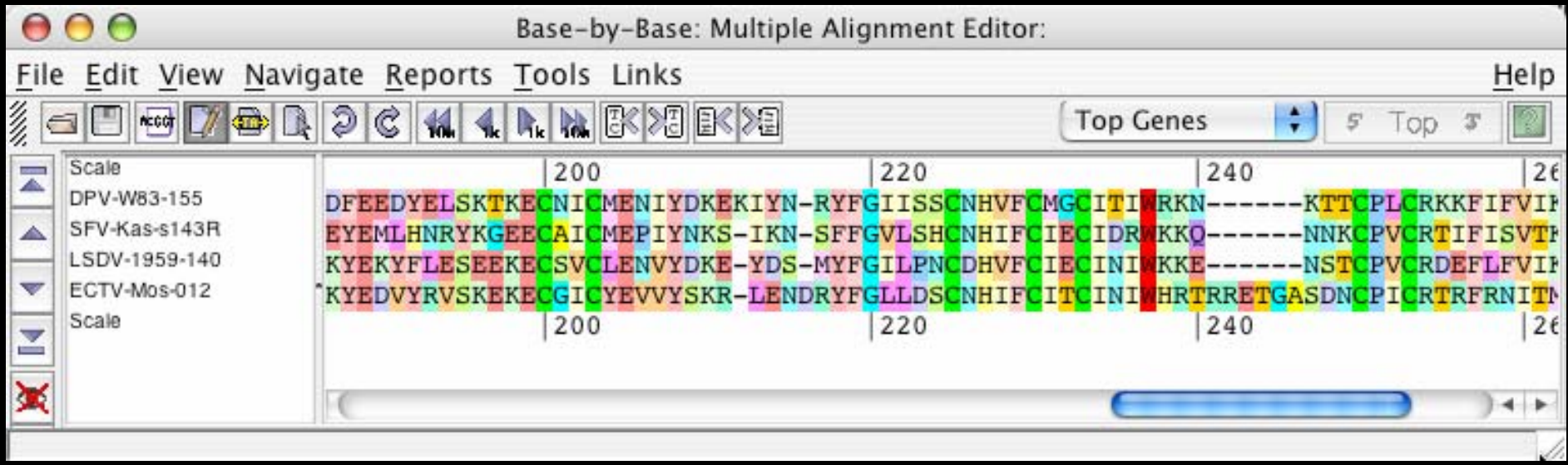

Sequence Map Display
File Analysis View Links
Help
Ectromelia virus (Moscow)
Go To: ECTV-Mos-001
Viewing Options...
Fuzzy Motif Search Results (TATACGACCGTGTTATAAATTAGGAGATA)
Top Strand GFS
Open Reading Frames
Start / Stop Codons
Top Strand Genes
ECTV-Mos-061
ECTV-Mos-064
ECTV-Mos-066
76000
76500
77000
77500
78000
78500
79000
79500
80000
80500
81000
81500
8200
Bottom Strand Genes
ECTV-Mos-062
ECTV-Mos-063
ECTV-Mos-065
Bottom Strand GFS
Start / Stop Codons
Open Reading Frames
Fuzzy Motif Search Results (TATACGACCGTGTTATAAATTAGGAGATA)
Base Data: AT Composition I Window Size:
91
95.60
66.82
45.5
95.60
45.5
%71.43
%67.3
Global Zoom
Auto-highlight Related Genes
Close
Ectromelia virus (Moscow) Now Active

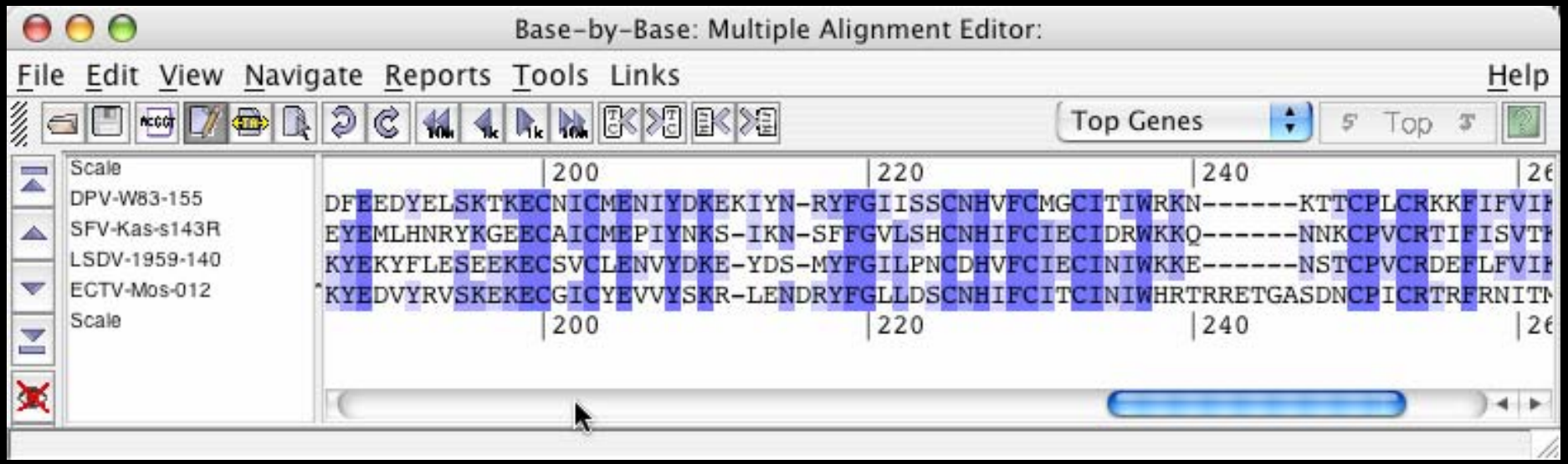

Multiple Sequence Map Display
File Analysis View Links
Help
Sequence Viewer (Cowpox virus (Brighton Red), Positive Strand)
Help
Close
Cowpox virus (Brighton Red)
Viewing Options...
Fuzzy Motif Search Results (TTTTT[ACGT]T)
Regular Expression Search Results (AGTACT)
Start / Stop Codons
Top Strand Genes
CPXV-BR-111
104000
104500
105000
105500
Bottom Strand Genes
CPXV-BR-110
CPXV-BR-112
Start / Stop Codons
Fuzzy Motif Search Results (TTTTT[ACGT]T)
Regular Expression Search Results (AGTACT)
Base Data: AT Composition I Window Size:
96.88
%64.0
68.60
44.0
%72.0
110000
CPXV-BR-1
%59.0
Ectromelia virus (Moscow)
Viewing Options...
ECTV-Mos-084
ECTV-Mos-087
ECTV-Mos-088
96000
96500
97000
97500
98000
98500
99000
99500
100000
100500
101000
101500
102000
ECTV-Mos-083
ECTV-Mos-085
ECTV-Mos-086
Global Zoom
Auto-highlight Related Genes
Close
CPXV-BR-111 selected , (Unknown (Cop-H2R))

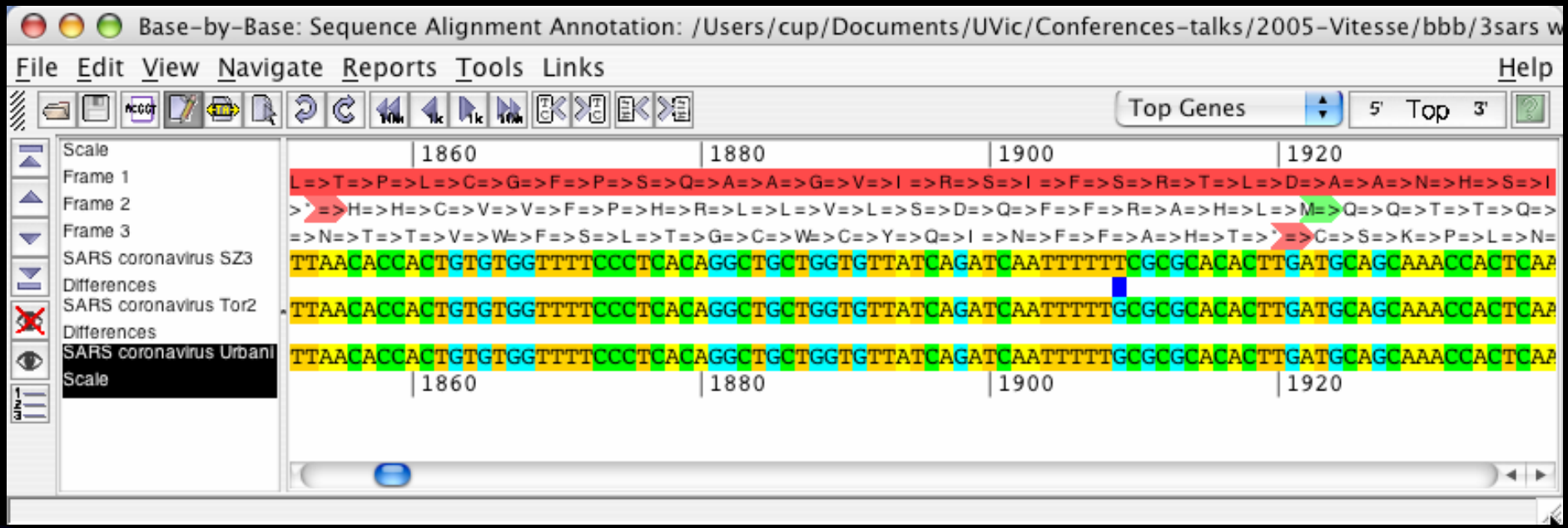

ECTV-Mos-085
File
Family Alignment
Analysis
Gene Info
Links
Help
Run PsiBlast
Run Blastp
Run Tblastn
Run MView
Family
On VOCs Database (HTML)
On VOCs Database (Text)
On NCBI (HTML)
On NCBI (Text)
Close

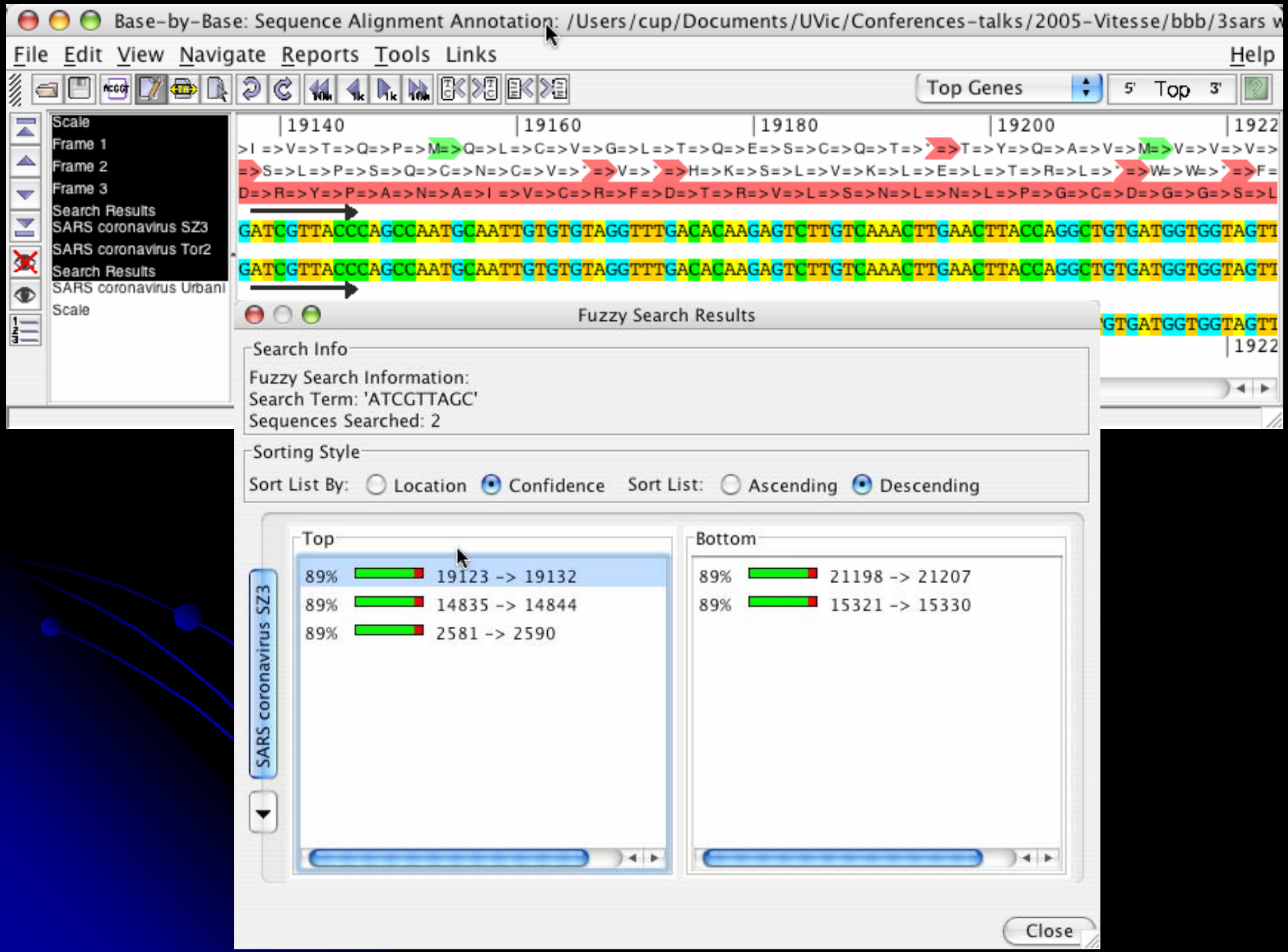
Base-By-Base: Genome Alignment

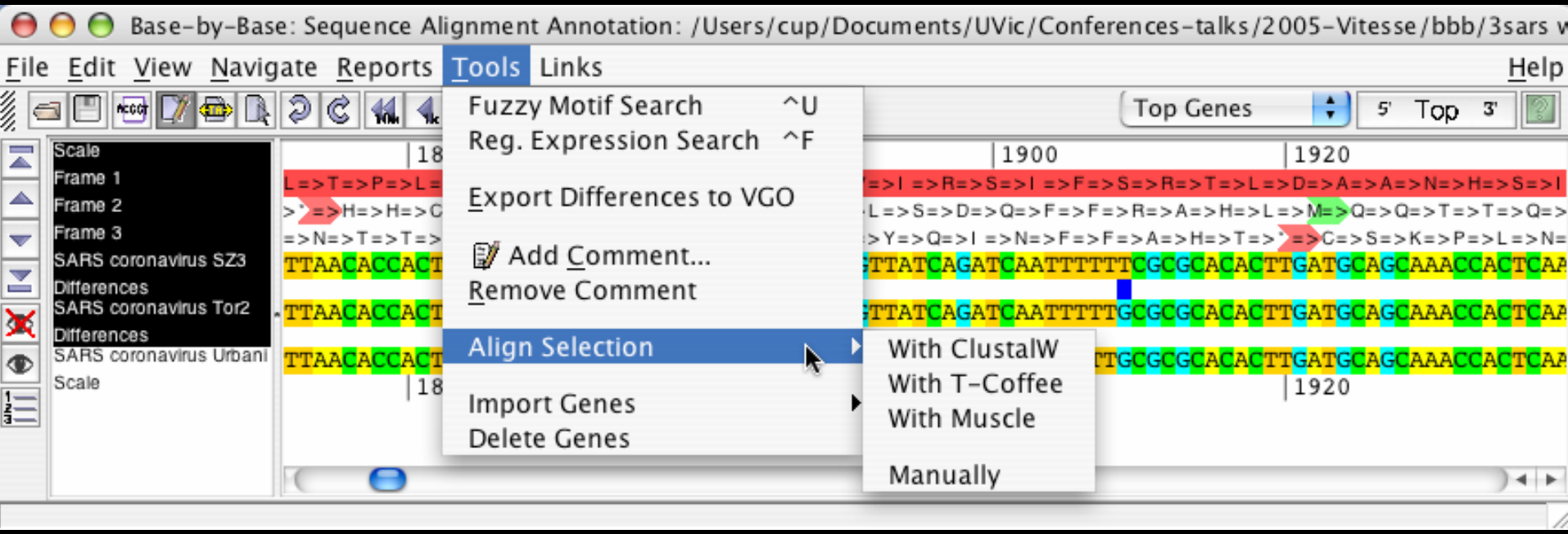
- Java MSA editor
  - Genes, proteins, genomes
  - Input from Clustal, Tcoffee, MUSCLE etc.
  - Uses XML format for annotations and comments
- Displays differences between sequences
- Finds all differences between genomes
  - Uses annotations from GenBank/VOCs
  - Lists diffs for each gene and 5’ region


Base-by-Base: Multiple Alignment Editor:
File Edit View Navigate Reports Tools Links Help
Top Genes
5' Top 3'
Scale
DPV-W83-155
SFV-Kas-s143R
LSDV-1959-140
ECTV-Mos-012
Scale
200
220
240
DFEEDYELSKTKECNICMENIYDKEKIYN-RYFGIISSCNHVFCMGCITIWRKN------KTTCPLCRKKFIFVIK
EYEMLHNRYKGEECAICMEPIYNKS-IKN-SFFGVLSHCNHIFCIECIDRWKKQ------NNKCPVCRTIFISVTK
KYEKYFLESEEKECSVCLENVYDKE-YDS-MYFGILPNCDHVFCIECINIWKKE------NSTCPVCRDEFLFVIK
KYEDVYRVSKEKECGICYEVVYSKR-LENDRYFGLLDSCNHIFCITCINIWHRTRRETGASDNCPICRTRFRNITN


Base-by-Base: Multiple Alignment Editor:
File Edit View Navigate Reports Tools Links
Help
Top Genes
5' Top 3'
Scale
DPV-W83-155
SFV-Kas-s143R
LSDV-1959-140
ECTV-Mos-012
Scale
200
220
240
DFEEDYELSKTKECNICMENIYDKEKIYN-RYFGIISSCNHVFCMGCITIWRKN------KTTCPLCRKKFIFVIK
EYEMLHNRYKGEECAICMEPIYNKS-IKN-SFFGVLSHCNHIFCIECIDRWKKQ------NNKCPVCRTIFISVTK
KYEKYFLESEEKECSVCLENVYDKE-YDS-MYFGILPNCDHVFCIECINIWKKE------NSTCPVCRDEFLFVIK
KYEDVYRVSKEKECGICYEVVYSKR-LENDRYFGLLDSCNHIFCITCINIWHRTRRETGASDNCPICRTRFRNITN


Base-by-Base: Sequence Alignment Annotation: /Users/cup/Documents/UVic/Conferences-talks/2005-Vitesse/bbb/3sars w
File Edit View Navigate Reports Tools Links Help
Top Genes
5' Top 3'
Scale
Frame 1
Frame 2
Frame 3
SARS coronavirus SZ3
Differences
SARS coronavirus Tor2
Differences
SARS coronavirus Urbani
Scale
1860
1880
1900
1920
TTAACACCACTGTGTGGTTTTCCCTCACAGGCTGCTGGTGTTATCAGATCAATTTTTTCGCGCACACTTGATGCAGCAAACCACTCAA
TTAACACCACTGTGTGGTTTTCCCTCACAGGCTGCTGGTGTTATCAGATCAATTTTTGCGCGCACACTTGATGCAGCAAACCACTCAA
TTAACACCACTGTGTGGTTTTCCCTCACAGGCTGCTGGTGTTATCAGATCAATTTTTGCGCGCACACTTGATGCAGCAAACCACTCAA


Base-by-Base: Sequence Alignment Annotation: /Users/cup/Documents/UVic/Conferences-talks/2005-Vitesse/bbb/3sars w
File Edit View Navigate Reports Tools Links Help
Top Genes
5' Top 3'
Scale
Frame 1
Frame 2
Frame 3
Search Results
SARS coronavirus SZ3
SARS coronavirus Tor2
Search Results
SARS coronavirus Urbani
Scale
19140
19160
19180
19200
1922
GATCGTTACCCAGCCAATGCAATTGTGTGTAGGTTTGACACAAGAGTCTTGTCAAACTTGAACTTACCAGGCTGTGATGGTGGTAGTT
Fuzzy Search Results
Search Info
Fuzzy Search Information:
Search Term: 'ATCGTTAGC'
Sequences Searched: 2
Sorting Style
Sort List By: Location Confidence Sort List: Ascending Descending
SARS coronavirus SZ3
Top
89% 19123 -> 19132
89% 14835 -> 14844
89% 2581 -> 2590
Bottom
89% 21198 -> 21207
89% 15321 -> 15330
Close


Base-by-Base: Sequence Alignment Annotation: /Users/cup/Documents/UVic/Conferences-talks/2005-Vitesse/bbb/3sars
File Edit View Navigate Reports Tools Links Help
Fuzzy Motif Search ^U
Reg. Expression Search ^F
Export Differences to VGO
Add Comment...
Remove Comment
Align Selection
Import Genes
Delete Genes
With ClustalW
With T-Coffee
With Muscle
Manually
Top Genes
5' Top 3'
Scale
Frame 1
Frame 2
Frame 3
SARS coronavirus SZ3
Differences
SARS coronavirus Tor2
Differences
SARS coronavirus Urbani
Scale
1900
1920

CDS Event Statistics

File View Links

Gene Na	Strand	ORF Sta	ORF Sto	Length	Aligned	Differen	Differen	Subs	Inserts	Deletes	200b Up	AA Cha	Silent Ch	Counter	Length	Length
SARS-S...	Top	12601	12939	339	339	0	0.00%	0	0	0	0	0	0	SARS-...	13149	-12810
SARS-S...	Top	28134	29402	1269	1269	0	0.00%	0	0	0	1	0	0	SARS-...	1269	0
SARS-S...	Top	28597	28809	213	213	0	0.00%	0	0	0	0	0	0	SARS-...	1269	-1056
SARS-S...	Top	9970	10887	918	918	0	0.00%	0	0	0	0	0	0	SARS-...	13149	-12231
SARS-S...	Top	28144	28440	297	297	0	0.00%	0	0	0	1	0	0	SARS-...	1269	-972
SARS-S...	Top	12007	12600	594	594	0	0.00%	0	0	0	0	0	0	SARS-...	13149	-12555
SARS-S...	Top	250	789	540	540	0	0.00%	0	0	0	0	0	0	SARS-...	13149	-12609
SARS-S...	Top	27258	27626	369	369	0	0.00%	0	0	0	0	0	0	SARS-...	369	0
SARS-S...	Top	27059	27250	192	192	0	0.00%	0	0	0	0	0	0	SARS-...	192	0
SARS-S...	Top	11758	12006	249	249	0	0.00%	0	0	0	0	0	0	SARS-...	13149	-12900
SARS-S...	Top	10888	11757	870	870	0	0.00%	0	0	0	0	0	0	SARS-...	13149	-12279
SARS-S...	Top	13357	13395	39	39	0	0.00%	0	0	0	0	0	0	SARS-...	13149	-13110
SARS-S...	Top	27623	27757	135	135	0	0.00%	0	0	0	0	0	0	SARS-...	135	0
SARS-S...	Top	13357	13383	27	27	0	0.00%	0	0	0	0	0	0	SARS-...	13149	-13122
SARS-S...	Top	12940	13356	417	417	0	0.00%	0	0	0	0	0	0	SARS-...	13149	-12732
SARS-S...	Top	19536	20573	1038	1038	0	0.00%	0	0	0	0	0	0	SARS-...	8088	-7050
SARS-S...	Top	26102	26332	231	231	0	0.00%	0	0	0	0	0	0	SARS-...	231	0
SARS-S...	Top	17955	19535	1581	1581	1	0.06%	1, 1 (1)	0	0	0	0	1	SARS-...	8088	-6507
SARS-S...	Top	790	2703	1914	1914	2	0.10%	2, 1 (2)	0	0	0	1	1	SARS-...	13149	-11235
SARS-S...	Top	13383	16151	2769	2769	3	0.11%	3, 1 (3)	0	0	0	1	2	SARS-...	8088	-5319
SARS-S...	Top	250	13398	13149	13149	15	0.11%	15, 1 (...	0	0	0	12	3	SARS-...	13149	0
SARS-S...	Top	250	13383	13134	13134	15	0.11%	15, 1 (...	0	0	0	12	3	SARS-...	13149	-15
SARS-S...	Top	13383	21470	8088	8088	9	0.11%	9, 1 (9)	0	0	0	3	6	SARS-...	8088	0
SARS-S...	Top	2704	8469	5766	5766	8	0.14%	8, 1 (8)	0	0	0	7	1	SARS-...	13149	-7383
SARS-S...	Top	16152	17954	1803	1803	3	0.17%	3, 1 (3)	0	0	0	1	2	SARS-...	8088	-6285
SARS-S...	Top	20574	21467	894	894	2	0.22%	2, 1 (2)	0	0	0	1	1	SARS-...	8088	-7194
SARS-S...	Top	25674	26138	465	465	1	0.22%	1, 1 (1)	0	0	3	1	0	SARS-...	465	0
SARS-S...	Top	26383	27048	666	666	2	0.30%	2, 1 (2)	0	0	0	1	1	SARS-...	666	0
SARS-S...	Top	8470	9969	1500	1500	5	0.33%	5, 1 (5)	0	0	0	4	1	SARS-...	13149	-11649
SARS-S...	Top	21477	25244	3768	3768	21	0.56%	21, 1 (...	0	0	0	18	3	SARS-...	3768	0
SARS-S...	Top	25253	26077	825	825	6	0.73%	6, 1 (6)	0	0	0	5	1	SARS-...	825	0
SARS-S...	Top	27764	28132	369	369	31	8.40%	2, 1 (2)	29, 29...	0	0	64	4	SARS-...	255	114
SARS-S...	Top	27764	28132	369	369	31	8.40%	2, 1 (2)	29, 29...	0	0	64	4	SARS-...	255	114

Report Data

GraphDNA: DNA Skew Graphing

VBRC

Orthologs

Similarity Search | Ortholog Comparison

search for shared gene orthologs

Select the appropriate parameters and press the **Submit** button
to get the set of all similar genes (orthologs) shared between the viruses in your list.

Submit Reset

Virus List	
Select viruses: (hold down the Ctrl key to make multiple selections)	Tick-borne encephalitis virus strain Vasilchenko Variola major virus strain Bangladesh-1975 Variola major virus strain India-1967 Variola minor virus strain Garcia-1966 Venezuelan equine encephalitis virus strain 243937
Protein BLAST comparisons between the above list of viruses should have:	
an E value less than	1e-4
and an alignment containing at least	90 **% identical residues.**

Matches are based on a BLAST search of all virus proteins in the VBRC database searched against the same protein set (an all-all search). BLAST parameters used include an E value cutoff of 0.0001 and no filtering of the query sequence.

Note that lowering the E value cutoff, or rasing the Percent Identical residues value will result in fewer hits - the BLAST search is more stringent.

- Mouse over a point to view a tooltip listing the represented genes.
- Click on a point to view the BLAST comparison results.

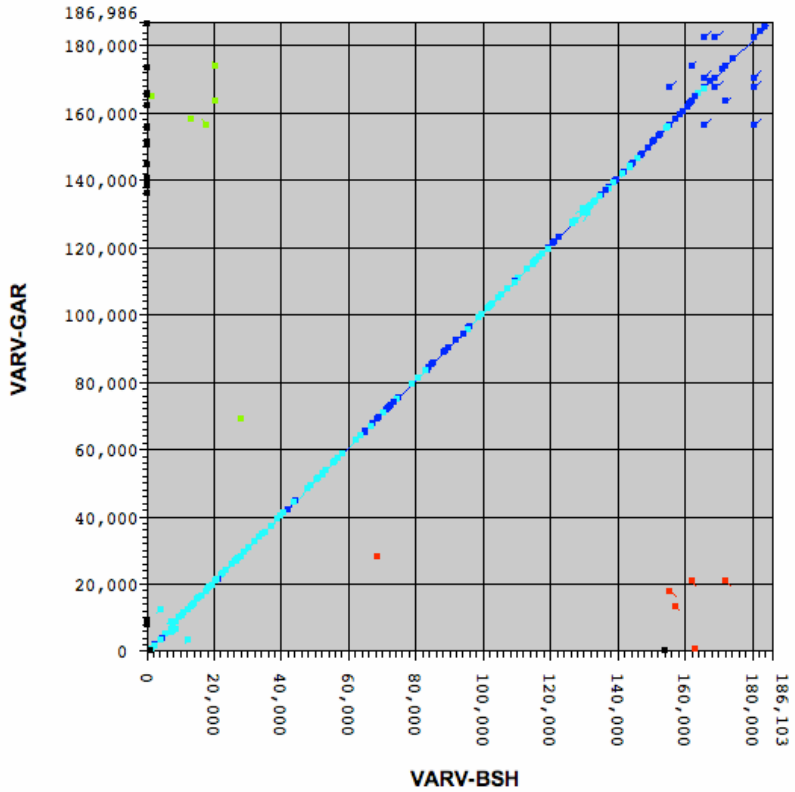
Zoom In

Gene Coding Strand: Genome on Horizontal / Vertical Axis

+/+
+/−
−/+
−/−
No Hits

ORF start — ORF end

Gene Synteny of Variola major virus strain Bangladesh-1975 vs. Variola minor virus strain Garcia-1966



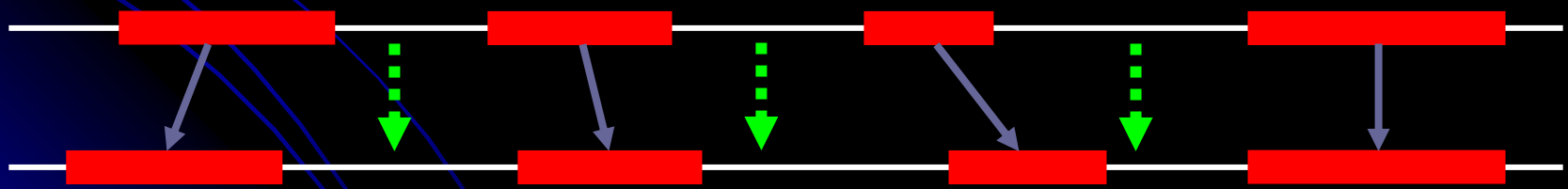
Generate GIF and SVG files of this plot.

E Value Cutoff

0.0 1.0E-100 1.0E-50 1.0E-25 1.0E-10 0.01

GenAlignRefine

- Refinement of multiple whole-genome alignments
- An initial alignment is generated with existing tools
  - Multi-LAGAN
  - CHAOS/DIALIGN
- Gapped (“fuzzy” regions) of the alignment are identified and refined (each to own compute node) to improve the overall quality of the entire alignment
  - Utilizes a genetic algorithm



Viral Bioinformatics Resource Center

& Viral Bioinformatics - Canada

University of Victoria

Workbench
- VOCS
- VGO
- Base By Base
- JDotter
- ReHAB
- GFS
- NAP
- GraphDNA
- Hydrophobicity
- Codon Statistics

Web Tools
- Laj Gallery
- BLAST
- EMBOSS

Information
- About Us
- About VBCa
- Virus Families
- Workbench
- Requirements

Welcome

This resource

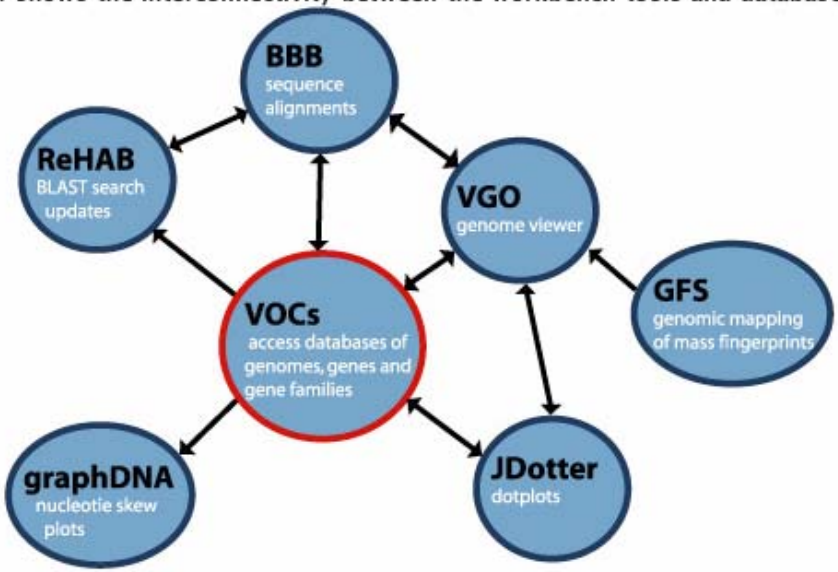
Provides access to viral genomes and a variety tools for comparative genomic analyses. At the heart of the system is VOCs (Virus Orthologous Clusters), a database with built-in tools that allows users to retrieve and analyze the genes, gene families, and genomes of 11 different virus families. The database is the source of information for other programs of the workbench for whole genome alignments, genome display, or gene/protein sequence analysis. Many of these tools can also be used with user-provided sequence data. The workbench tools are Java-based and user-friendly to allow all users, regardless of computer skill-level, to access and analyze the data.

To start

There are two ways to start an application from the workbench:

- Select an application, and then choose its associated database when the application starts.
- Select a database, and then start an application using the afore-selected database.

The figure below shows the interconnectivity between the workbench tools and databases at VBCa



Databases

dsDNA viruses
- Adenoviridae
- Baculoviridae
- Herpesviridae
- Poxviridae

+ ssRNA viruses
- Coronaviridae
- Flaviviridae
- Togaviridae

- ssRNA viruses
- Arenaviridae
- Bunyaviridae
- Filoviridae
- Paramyxoviridae

Bacterial plasmids
- Plasmids

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